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                                               pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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Sequence 1 from Patent DE19847779.
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                                                                                   Eukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3212)
1 (bases 1 to 3212)
Nueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating Novel receptor dna useful for cancer chemotherapy substances potentially useful for cancer chemotherapy substances potentially useful for cancer chemotherapy substances potentially useful for cancer chemotherapy patent. DE 1947779-C 1 03-FEB-2000; Patent. DE TREBSFORSCH (DE)
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## 당 DEFINITION AL157394 ACCESSION REFERENCE SOURCE KEYWORDS COMMENT ORGANISM JOURNAL AUTHORS FEATURES Direct Submission 2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK E-mail enquiries; humquery@sanger.ac.uk Clone requests: Clonerequestesanger.ac.uk replaced gi:14161146. The puring sequence assembly data is compared from overlapping clones. On Aug 31, 2001 this sequence version replaced as variations of the overlapping clone name. Note that the puring sequence assembly data is compared from overlapping clone saw an anotation annotation may not be found in the sequence submission where was an anotation any otherwise noted: all corresponding to the overlapping clone, as we submit sequences with together with overlap as described above. This sequence was finished as follows unless otherwise noted: all corresponding to the overlapping data (i.e., phred quality >= the sequence was finished as follows unless otherwise noted: all regions were either double-stranded of ata (i.e., phred quality >= the sequence was finished as follows unless otherwise noted: all regions were either double-stranded of ata (i.e., phred quality >= the sequence was finished as follows unless otherwise noted: all regions were covered by high quality data (i.e., phred quality >= the sequence was finished to resolve all sequencing problems, such regions were either double-stranded or all subclone; and the as compressions and repeats; all regions were covered by the least one phasmid subclone or more than one M13 subclone; and the as compressions are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL: Sw:, assembly was core table with their source databases: BASE COUNT ORIGIN Query Match Best Local Similarity source 187313 bp DNA linear PRI AL157394 uman DNA sequence from clone RP11-399019 on chromosome misc\_feature complete sequence. AL157394 misc\_feature misc\_feature misc\_feature AL157394.15 GI:15384622 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; http://www.sanger.ac.uk/projects/C\_elegans/wormpep This sequence http://www.sanger.ac.uk/projects/compep This sequence http://www.sanger.ac.uk/projects/compep This sequence http://www.sanger.ac.uk/projects/compep This sequence http://www.sanger.ac.uk/projects/compep This sequence http://www SWISSPROT: Tr. TREMBL; Wp:, WORMPEP; database can be found at \_\_\_\_\_\_ (bases 1 to 187313) http://www.sanger.ac.uk/HGP/Chr10 RP11-399019 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see This sequence is the entire insert of clone RP11-399019 The true this sequence RP11-499H23 is at 166408 in this sequence. The left end of clone RP11-30415 is at 18704 in this sequence. true right end of clone RP11-30415 is at 18704 in this sequence. of Pieter de Jong. For rurcher de htm http://www.chori.org/bacpac/home.htm Location/Qualifiers /organism="Homo sapiens" /db\_xref="taxon:9606" /clone="RP11-399019" /clone\_lib="RPCI-11.2" /chromosome="10" /note="Sequence from AC015461 sequenced by WIBR." 105808. 105972 100119 /note="Sequence confirmed by AC015461 sequenced by WIBR." 100157. 100198 note="Sequence from AC015461 sequenced by WIBR." 99.2%; 99.7%; score 3185; pred. No. 0; DB 9; Length 187313; PRI 22-AUG-2001

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Db 142989 GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTA 143048
                                  Db 142929 Grearggaaagecereaggaaggraaceraaceragarttgaaggececaaacaggereca 142988
                                                                    Qy 901 acaagcctatcaacacctacaagactggtggtaagtgcagtgacagatgcaaacacagg 960
Db 142869 ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG 142928
                                                                                                       Db 142809 GGCTGGCACGCCCAGGGTCTTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG 142868
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Db 142749 TACCATCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA 142808
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Db 142209 CTAAGATTATTTGACCATGAAACATATGTCTCCCCACAAAGCACATATTCCTATCTCCTT 142268
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                                                                                        145089 AACCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCTGTTTTGAAAAAGTCCCTCGCT 145148
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2827)

Nueller-Schilling,M., Krammer,P. and Oren,M.

Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 4 03-FEB-2000; Patent: DE 1984779-C 4 03-FEB-2000;
                                                                              2827 bp
Sequence 4 from Patent DE19847779.
AX026092
                                                       541 cacatatgtgagttgctggcttataattcacactcaagagatactgattttgtcaattgt 600
541 CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT
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721 attttggaatagt 721 attttggaatagt 721 attttggaatagt 1                   721 arTTTGGAATTAGT 781 taccatcctctt 1                781 TACCATCCTCTTT 781 taccatcctctt 1                841 GGCTGGCACGCCCA 841 GGCTGGCACGCCCA 901 acaagcctatcaac 901 acaagcctatcaac 1                  841 GGCTGGCACGCCA 901 acaagcctatcaac 1                  841 GGCTGGCACGCCA 901 acaagcctatcaac 1                         841 GGCTGGCACGCCA 901 acaagcctatcaac 1                         841 GGCTGGAAGCCAATCCAAC 1	toacaccottttocttccttctttttacattttttattta
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2; Indels 1; Gaps 1;

Query Match 68.9%; Score 2211.8; DB 9; Length 2344;	<u>.                                  </u>	misc_signal 717801 interferon silencer B motifs"  /note="beta interferon silencer B motifs" /note="beta interfe	/germline /tissue_type="placenta" /map="4024.1" misc_signal 564.1337 f64.1337	Ce	TITLE Direct Submission TITLE Direct Submission JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAND JOURNAL Submitted (26-May-1995) F.H. Rudert, Genesis Research & ZEALAN	DNA CELL BLUL IT VIII 96069539 2 (bases 1 to 2344) Rudert,F.H.	Watson, J. Identificat in the hum	Eukaryota; Metazoa; Cibrucc, Catarrhini; Hominidae; Homon Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homon Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homon Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homon Mammalia; Hominidae; Homon Mammalia; Hominidae; Homon Mammalia; Hominidae; Homon Mammalia; Hominidae; Homi	x87625.1 GI:902311 beta interferon; CD95 gene; silencer. human. human sapiens	RESULT 4 HSCD955FR HSCD955FR 2344 bp DNA linear PRI 05-FEB-199/ LOCUS DEFINITION H.sapiens CD95 gene 5' flanking region.  DEFINITION H.Sapiens CD95 gene 5' flanking region.	CAGAAATGCCAGCTTGCAGATGGCTAATCAAAAA 2020	Db 2728 AACCCGGCGCCTATTATTGGCCAAGAAACTIGAGGCCCCCCCCCC	Db 2668 CCATGGTGATTTCTGCTAGGTGATTTCTGCT 3179  OP 3120 aacccggcgcctattattggccaagaaacttgagcagcctgttttgaaaaagtccctcgct 3179  OP 3120 iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	Ob 2608 CATTTTGTTTTAGTTTTAGTTGTTGTTGTTGTTGTTGTTGT	GCCTTGTCCCTTC-GGCCTTCTCTTTCTTTTGCCCTTTCTTAGCTTGCACTC		GGTIAANOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO	TO THE ACCOMMENTATION OF THE PROPERTY OF THE P
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2218 GCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTTCTCCCGC 2277
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66.7%; Score 2143.4; 99.7%; Pred. No. 0;

DB 9; 6,

Length 2165;

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Query Match
Best Local Similarity 93...
2158; Conservative
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Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University,
Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa,
Ishikawa 920-0934, Japan (E-mail:nakanaka@dbs.p.kanazawa-u.ac.jp,
Te1:076-234-4424, Fax:076-234-4480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vakanishi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection. Chem. 270 (30), 18007-18012 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2380)
Mueller-Schilling, M., Krammer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating Patent; DE 19847779-C 3 03-FEB-2000;
DEUTSCHES KREBSFORGH (DE)
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/usedin=x81336.1:155	/_abel=Hinkxxx-1" /product="APO-1" /product="APO-1" 16891810 16891810 /gene="API" /gene="API" /label=ex1c /number=1.7335.HsmRNA3 /number=1.7375.HsmRNA3 /number=1.7375.HsmRNA3	/gene="AFT" /Jabel=HsmRNA2 /Jabel=HsmRNA2 /Jabel=HsmRNA2 /product="APO-1" /product="APO-1" Join(1689) . 1810, x81336.1:155320, x81339.1:766828, join(1689) . 1810, x81339.1:552613, x81399.1:765. x81338.1:145253, x81399.1:552279, x81342.1:1031757) x81340.1:79161, x81341.1:255279, x81342.1:103757) /gene="APT" /gene="APT"	/number=1 /numbe	/number=1335:HsmRNA1 /usedin=X01335:HsmRNA1 /usedin=X013135:HsmRNA1 /usedin=X01 /iffication=1APT /usedin=APT /usedin=X01 /usedin=X01 /usedin=X01	16531810 exon /gene="APT" /label=exla	/gence "AFF" AFF"  /label=HanRNAI   /label=HanRNAI   /product="APP"   /pro	misc_feature /151. 261 / 125		Heidelberg, ""  FEATURES 1.1877  Source /organism="Homo sapiens"  source /organism="Homo sapiens"	MEDILINE 25104292 MEDILINE 251	MAMMALIA: 100 1897)  REFERENCE 1 (Dases 1 to Alczak H. and Krammer, P.H.  AUTHORS Behrmann I., Walczak H. and Krammer, P.H.  Structure of the human APO-1 gene Structure of the human APO-3062 (1994)  TITLE FUT. J. Immunol. 24 (12), 3057-3062 (1994)	ACCESSION X81335.1 GI:537410 VERSION X81335.1 gene; apt gene. KEYWORDS human. SOURCE Homo sapiens ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.	Db 2368 TCAAAG 2373

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X81340.1:79. .161,X81341.1:255. .279,X81342.1:103. .1757)
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47.8%; Score 1536.8; 98.6%; Pred. No. 0; 98.6%; Pred. No. 0; Mismatches o; Mismatchest accatectecttateceatectect[	ens" "1 genomic 1 1 genomic 366 t	E human Fas gene ), 1239-1245 (19 8) 8) 701 South 19th S 704 O007, USA M67454 and X637 Qualifiers	1608 bp DNA 3, Apo-1 gene (promoter and 1:673405 FAS gene. etazoa; Chordata; Craniata theria; Primates; Catarrhi to 1608)	agtgacttggctggagcctcagggggggcactggcacggaacagccctgaggcaggc
DB 9; Length 1000,  17; Indels 5; Gaps 3;    11    1  1  1  1  1  1  1  1  1  1  1	DNA"	(Alabama at B	l linear PRI 17-FEB-1995 [exon I). [vertebrata; Euteleostomi; hominidae; Homo. [ntz.J.D.]	pacacctdgagccagcc

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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181 c 216 g 18:
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100.0%; Pred. No. 1.9e-155;
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Direct Submission
Submitted (19-SEP-2000) Muschen M., Department of Immunology,
Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                                                                                     Related sequences: D31968 X89101 AJ279011 AJ279013
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Kuppers,R. and Rajewsky,K.
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1 (bases 1 to 702)
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AJ279012
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702 bp DNA linear PRI 02-APR-20 HSA279012
HOMO Sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon
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282. .>313
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/db_xref="taxon:9606"
/cell_type="Reed-Sternberg cells"
/note="Hodgkin's disease tissue-polymorphic allele (+275)"
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                                                                             Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon
Muschen,M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 702)
                                                    Apo-1 Fas; CD95 antigen; CD95 gene.
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2246 tcctacctctggtgatccctctcctgcccgggtggaggcttaccccgtcttagtcccggg 2305
                                           181 CTGGCTGCCCAGGCGGAGCTGCCTCTTCTCCCGCGGGTTGGTGGACCCGCTCAGTACGGA
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Muschen, M., Re, D., Brauninger, A., Wolf, J., Hansmann, M.L., Diehl, V., Kuppers, R., and Rajewsky, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9,
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pred. No. 9.1e-152;
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                                                                                                                                                                                                                                                                                                           Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9,
                                                                                                                                                                                                                                                                               Related sequences: D31968 X89101 AJ279011 AJ279012.
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Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ279013.1 GI:13539242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 702)
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                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                    RESULT 1
BC012479
LOCUS BC012479 2719 bp mRNA linear PRI DEFINITION Homo sapiens, Similar to tumor necrosis factor receptor
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                                                                                                                                                            601 CTGCGCTCCACGTTGAGGTGGGCATGGGGGGCGGACAGGAATTGAAGCGGAAGTCTGGGA
                                                                                                                    2606 agctttagggtcgctggagggggaccccggttggagagagga 2647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 698;
                                                                                                                                                                              2546 ctgcgctccacgttgaggtgggcgtgggggggggacaggaattgaagcggaagtctggga 2605
                                                                                                                                                                                                                                           2486 tgatgcgaagtgctgatcccgctgggcaggcggggcagctccggcgctcctcggagacca 2545
                                                                                                  2426 taggacettccetcaggeccgggfgctcagaacgatggaggacttgctttcttgggcct 2485
                                                                                                                                                                                                                                                                                                                                                                            2366 gggcacctgggagcggggtgctgctgcgggaggcgttggagactggctcccggggggctgt 2425
                                                                                                                                                                                                                            541 TGATGCGAAGTGCTGACCCCGCTGGGCAGGCGGGCAGGCTCCTCGGGAGACCA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                           2306 gataggcaaagtggggggggggggggacgcgtgcgggattgcggcgggcagcggcgcacgc 2365
                                                                                                                                                                                                                                                                                           481 TAGGACCTTCCCTCAGGCCCGGGTGCTCAGAACGCTGGAGGACTTGCTTTTCTTTGGGCCT 540
                                                                                                                                                                                                                                                                                                                                                          421 GGCACCTGGGAGCGGCGGCTGCTGCGGGAGGCCTTGGAGACTGGCTCCCGGGGGGCTGT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2186 gttggggaagctctttcacttcggaggattgctcaacaaccatgctgggcatctggaccc 2245
                                                                                                                                                                                                                                                                                                                                                                                                                             361 GATAGGCAAAGTGGGGCGGGGCGCGGGACGCGTGCGGGATTGCGGCGGCAGCGGCACGGCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2126 ctggctgcccaggcggagctgcctcttctcccgcggggttggtggacccgctcagtacgga 2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2066 agtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagcc 2125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CTGCCTGCCCAGGCGGAGCTGCCTCTTCTCCCGCGGGGTTGGTGGACCCGCTCAGTACGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGGCACGGGAACACCCCTGAGGCCCAGCC 180
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SOURCE KEYWORDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2719)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I M.A.G.E. Consortium (DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg, R
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ggcttttcgtgagctcgtctctgatctcgcgcaagagtgacacacaggtgttcaaagacg 2036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov geries: IRAK Plate: 28 Row: i Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                           342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: villalon@bcm.tmc.edu.
villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AAQ93879
AAX24878
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                                                Human colon cancer
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DNA encoding a hum
Fas-delta-TM cDNA.
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AAT34530
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AAZ23892
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EP-892047 Seq ID 4
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## ALIGNMENTS

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Matches 1582;
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                                                                                                                            A novel DNA segment (AAT34162) has an isolated sequence region defined as the Fas gene promoter region. This includes a number of transcription factor binding sites. A coding sequence for latent partion (AAR99471) of the Fas protein leader peptide corresponding to nt 23-246. It can be combined with a structural transcription factor binding sites. The promoter region can be completed from a means of treating Fas mediated apoptosis disorders such as means of treating Fas mediated apoptosis disorders such as
827 gagtgtgtgcacaaggctggcacgcccagggtcttcctcatggcactaacagtctactga 886
                   Sequence 1608 BP; 398 A; 421 C; 423 G; 366 T; 0 other;
                                                                                                                                                                                                                                                     Claim 11; Fig 2; 123pp; English.
                                                                                                                                                                                                                                                                       Human Fas gene promoter region - used for heterologous protein expression and for developing products for treating Fas mediated
                                                                                                                                                                                                                                                                                                                P-PSDB; AAR99471.
                                                                                                                                                                                                                                                                                                                                         Cheng J, Koopman WJ,
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                                                                      Similarity 98.6
82; Conservative
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                                                                             47.88;
98.68;
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/note- "5' end of intron 1 (full length approx.
14 kb"
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/product= Fas protein leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function= CP2 transcription factor binding site
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/note= "claim 5"
1037..1043
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/note=_"claim 7"
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                                                                Score 1536.8;
Pred. No. 0;
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1027 gtgag-atgccagccactgcaggaacgccccgggacaggaatgcccatttgtgcaacgaa 1085
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                                                                                                                                                                  967 gaactacagcagaagcetttagaaagggcaggaggceggctctcgaggtcctcacctgaa 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic; Human; immune system disease; cytosine methylation; notropic; antiarteriosclerotic; antianaemic; cytostatic; nobthalmological; antiarteriosclerotiv; antiforwulsant; ophthalmological; antirbeumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; antiabetic; antipsoriatic; antiarthritic; antiarthritic; antidiabetic; antipsoriatic; anaemia; antinflammatory; cancer; eye disease; arteriosclerosis; epilepsy; antificiamatory; cancer; eye disease; arteriosclerosis; epilepsy; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; antiinflammatory; eye disease; arteriosclerosis; anaemia; antiinflammatory; eye disease; arteriosclerosis; anaemia; antiinflammatory; eye disease; arteriosclerosis; anaemia; a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 2392.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            03-JAN-2002.
                                                                                                                                                                                                                                                   30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                  02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG.
                                    Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal for diagnosis and treatment of diseases associated with abnormal for diagnosis and treatment of diseases associated with abnormal for diagnosis and treatment of diseases.
Claim 1; SEQ ID NO 2392; 32pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                              1242 TracanaarahaarahahacrianarahacGaraccanaanaratacranaanccriraara 1183
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                                                                                                                                                                                                                                                           1186 tgtccagtctggaactgcatocaaattcaggtcagtaatgatgtcattatccaaacata 1245
                                                                                                                                                                                                                                         1182 TATCCAATCTAAAACTACATCCAAATTCAATTCAATTAATATATCATTATCCAAACATA 1123
                                                                                                                                                                                                               1246 ccttctgtaaaattcatgctaaactacctaagagctatctaccgttccaaagcaatagtg 1305
                                                                                                                                                                                                      1122 CCTTCTATABAATTCATACTAACTACCTABAAAACTATCTACCGTTCCAAAAAACAATAATA 1063
                                                                                                                                                                            1366 ggccaggaataatgagtaacgaaggacaggaagtaattgtgaatgtttaatatagctgg 1425
                                                                                                                                                                  1002 AACCAAAAATAATAATAACGAAAAAACAAAAATAATTATAAATATTTAATATAACTAA 943
                                                                                                    1426 ggctatgcgatttggcttaagttgttagctttgttttcctcttgagaaataaaaactaag 1485
                                                                       1486 gggccctcccttttcagagccttatggcgcaacatctgtactttttcatatggttaactg 1545
                 882 AAACCCTCCCTTTCAAAACCCTATAACGCAACATCTATACTTTTTCATATAATTAACTA 823
1605 aaatgccccgcaagtctttctctgagtgactccagcaattagccaaggctcctgtaccca 1665
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76.68;
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RESULT
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Human; immune system disease; cytosine methylation; antiasthmatic; neuroprotective; anti-Hry, antianemic; cytostatic; nootropic; anti-Hry, anticonvulsant; ophthalmological; antirheumator; cancer; eye disease; arteriosolerosis; aneurofibromatosis; rheumatoid arthritis; antidiabetic; antipsoriatic; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease, arman, a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               642 AAACTACAACAAAACCTTTAAAAAAAAAAAAAAACGACTCTCGAAATCCTCACCTAAA 583
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499 ttlatgitaaattaittaagagitaittaitegiittaaagitaatagigattitgaatagi 558
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                                        439 aattytätttääätttägytttäytäätyätyttättätttääätättttttytääää 498
                                                                                           1138 gtgcagaggttggtggacgatgccaaaggaatactgaaacctttagtgtgtccagtctgg 1197
                                                                               379 gtgtagagtttggtggacgatgttaaaggaatattgaaatttittagtgtgtttagittgg 438
                                                                                                                                   1078 tattaatgtgttattaatgggttgaatctaattgggaagggagagggttgcagagtgag 1137
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                                                                                                                                                              259 tagaagaaaatgitaattgagaggaagtttgaaggatgaatagtgggttaagtaaagggt 318
                                                                                                                                                                                                                                                                                                                                                                                                   Matches 1215; Conservative
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                                                                                                                                                                                                       959 999tgatggaaagccctcaggagggtaacctaacctagatttgaggg-cccaacaggctc 1017
                                                                                                                                                                                                                                              139 agataagtttattaatatttataagattggtggtaagtgtagtgatagatgtaaaatata 198
                                                                                                                                                                                                                                                           899 agacaagcotatcaacacctacaagactggtggtaagtgcagtgacagatgcaaaacaca 958
                                                                                                                                                                                                                                                                                                    839 aaggetggeacgeecagggtetteeteatggeactaacagtetaetgaaaggtggaacag 898
                                                                                                                                                                                                                                                                                      79 aaggitggtacgtttagggtttttttttatggtattaatagtttattgaaaggtggaatag 138
                                                                                                                                                                                                                                                                                                                                          779 tataccatcotocttatoccacttotttttgtgtotattagatgctcagagtgtgtgcac 838
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of human immune system associated can be used in the diagnosis and treatment of fumune system associated incular degeneration, arterioscierchia, neovascular glaucoma and teukamia, Alzheimer's disease, ANDS, epissy, neovascular glaucoma and diseases. The present sequences in the system of arthritis, psoriasis and infilammatory, neurofibromatosis, disease. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1608 BP; 398 A; 51 C; 423 G; 736 T; 0 other;
                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2391; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-130909/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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Similarity 29.8%; Score 957.4; DB 24; Length 1608;
15; Conservative 0; Mismatches 371; Indels 5;
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1575 gcgggattgcggcggtacggcgtatcgcggg 1605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                gccactgcaggaacgccccgggacaggaatgcccatttgtgcaacgaaccctgactcctt 1857
                                                                                                                                                                                                                                                                                                                                                                                                        aagttittagaaagggtaggaggtcggttttcgaggtttttatttgaagtgag-atgtta 1037
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                                                                                                                                                                                                                                                                                   ttttattttgattttttttttttttattcgcgcgtaggttaägttgttgaattaatgga 1157
                                                                                                                                                                                                    gcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggaggattgc 2217
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                                                                                                                                                                        tggcacggaacacccctgaggccagccctggctgcccaggcggagctgcctcttctccc 2157
                                                 gcgggattgcggcggcagcggggcacgcgggg 2368
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunomodulatory; muscular; gynaecological; gastrointestinal;
nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
                                                                                                                                                         Matches
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identification; cytostatic; cardioactive; neuroprotective; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200055351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2000; 2000WO-US05883.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The called human colon cancer antigens can have cytostatic, cardioactive, muscular; human colon cancer antigens can have cytostatic, cardioactive, muscular; human colon cancer antigens can have cytostatic, gastrointestinal, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and vulnerary, nephrotropic, antiinfective and antibacterial activities, and research the prevention, can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibacdies to the proteins are useful for the prevention. The treatment and diagnosis of colon disorders, such as colon cancer. The treatment and diagnosis of colon disorders, such as colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 610-611; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB53420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
                                                                                                                                                                                                                                                                                                         polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins chromosome identification, and as hybridisation probes. The proteins chromosome identification, and as hybridisation probes. The proteins system disorders, muscular disorders, reproductive disorders, system disorders, muscular disorders, renal disorders, infectious gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB64007 represent sequences used in the exemplification of the present apa64007 represent sequences used in the exemplification.
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                                                                                                                                                                                                                                                     Sequence 859 BP; 214 A; 219 C; 227 G; 193 T; 6 other;
                                                                                              1954 cttcccatcctcctgaccaccggggcttttcgtgagctcgtctctgatctcgcgcaagag 2013
                                                                                                                                                                                                                                                                                              invention.
                   2014 tgacacacaggtgttcaaagacgcttctggggagtgaggggaagcggtttacgagtgactt 2073
                                                                                 19
                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-587534/55.
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                                                                          cgtccgcccacgcgtccgaccggggcttttcgtgagctcgtctctgatctcgcgcaagag
tgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacgagtgactt 138
                                                                                                                                                                294;
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                                                                                                                                                              Conservative
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                                                                                                                                                                                         96.4%;
                                                                                                                                                                                                           8.9%;
                                                                                                                                                                                         Score 287.4; DB : Pred. No. 1.5e-67
                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                 DB 21; Length 859;
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Matches 264;
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Best Local
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AAZ88700
            2500 gatcccgctgggcaggcggggcagctccgggcgctcctcggagaccactgcgctccacgtt 2559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ъ
                                                                                                                                       This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor intron 1 which contains a p53 bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     γQ
                                                                                                              Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                      region described in the method of the invention.
                                                                                                                                                                                                                        Claim 2; Fig 4; 12pp; German.
                                                                                                                                                                                                                                     Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy -
                                                                                                                                                                                                                                                                                      WPI; 2000-162245/15.
                                                                                                                                                                                                                                                                                                                            (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
1 gatcccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgtt 60
                                                                                                                                                                                                                                                                                                                                                             16-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                DE19847779-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CD95 receptor intron 1 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ88700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ88700 standard; DNA; 266 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2194 agetettteaetteggaggattgeteaacaaecatgetgggcatetggaccetectacet 2253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2254 ctggt 2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 agctctttcacttcggaggattgctcaaccaaccatgctgggcatctggaccctcctacct 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2074 ggctggagcctcagggggcggggcactggcacggaacacaccctgaggccagccctggctgc 2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 ctggt 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199
                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccaggoggagctgoctottctcccgcgggttggtggacccgctcagtacggagttgggga 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ccaggcggagctgcctcttctcccgcgggttggttggtqgacccgctcagtacggagttgggga 2193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99ctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccctggctgc 198
                                                               Conservative
                                                                                                                                                                                                                                                                                                      Mueller-Schilling M,
                                                                                                                                                                                                                                                                                                                                                        98DE-1047779.
                                                                                                                                                                                                                                                                                                                                                                             98DE-1047779.
                                                                        8.2%;
99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 160..179
                                                                                                                                                                                                                                                                                                                                                                                                                                               bound_moiety= p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                       Score 262.8; pred. No. 3.5e.0; Mismatches
                                                              ,0
                                                                                                                                                                                                                                                                                                      Oren M;
                                                                   3.5e-61;
                                                                      _ DB_21; Length 266;
                                                       <u>ب</u>
                                                  Indels
                                                                                                                                         a p53 binding
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Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;

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XX DT XX
       The present sequence encodes human Fas (Apo-1). The specification describes antisense compounds which are targeted to the 5'-untranslated region, translational start site, translational termination region of 3'-untranslated region of nucleic acid molecules encoding Fas, Fas phosphatase). The antisense compounds are used to inhibit the expression of Fas, Fast or Fap-1 in cells or tissues. They are used to treat autoimmune or inflammatory diseases such as hepatitis. They can also be used to treat cancer, especially colon, liver or lumphorms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC61798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΨ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                       Example 2; Page 71-73; 116pp; English.
                                                                                                                                                              Antisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
                                                                                                                                                                                                                     P-PSDB; AAB19341.
                                                                                                                                                                                                                                                                           (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                       10-APR-2000; 2000WO-US09540
                                                                                                                                                                                                                                                                                                      12-APR-1999;
                                                                                                                                                                                                                                                                                                                                                   19-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                         WO200061150-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease; inflammatory disease; lymphoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding a human Fas (Apo-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC61798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC61798 standard; DNA; 2551 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2740 gagcctacagccttcagaacacatat 2765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2620 tggagggggaccccggttggagagaggagcggaactcctggacaagccctgacaagccaa 2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 gagoctgcagcottcagaacagatat 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2560 gaggtgggggggggggggacaggaattgaagcggaagtctggggaagctttagggtcgc 2619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 tggaggggaccccggttggagagaggagcggaactcctggacaagccctgacaagccaa 180
                                                                                                                                                                                                                              2000-628395/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9a99t999c9t999999c9gacaggaattgaagcggaagtctgggaagctttagggtcgc 120
                                                                                                                                                                                                                                                     Marcusson EG;
                                                                                                                                                                                                                                                                                                99US-0290640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein 1; protein tyrosine phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                            /product= "Fas"
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer;
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Query Match 7.8%; Score 252; DB 21; Length 2551; Best Local Similarity 100.0%; Pred. No. 1.2e-57; Best Local Similarity 0; Mismatches 0; indels 0; Matches 252; Conservative 0; Mismatches 0; indels 0;

0

Gaps

2007 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggagtggggtttacga 2066

1 gcaagagtgacacacaggtgitcaaagacgcttctggggagtgagggaagcggtttacga 60

2067 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 2126

61 gtgacttggctggagcctcaggggcggggcactggcacggaacacaccctgaggccagccc 120

2127 tggctgcccaggcggagctgcctcttctcccgcgggttggtggacccgctcagtacggag 2186

tggctgcccaggcggagctgcctcttctcccgcgggttggtggacccgctcagtacggag 180

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В

g Š

2247 cctacctctggt 2258

cctacctctggt 252

AAQ93879;

06-NOV-1995 (first entry)

Fas-delta-TM CDNA.

Fas-delta-TM; transmembrane deletion; apoptosis; antibody;

adoptive immunotherapy; transgenic animal; ss.

Homo sapiens.

Location/Qualifiers

AAQ93879 standard; cDNA; 2471 BP

7

W09513701-A. 26-MAY-1995

(LXRB-) LXR BIOTECHNOLOGY INC.

Barr PJ, Kiefer MC,

Shapiro JP;

p-psdB; AAR76238. WPI; 1995-200120/26.

Claim 3; Fig.3-1 to 3-4; 38pp; English.

15-NOV-1993; 15-NOV-1994;

94WO-US13173.

93US-0152443.

mat\_peptide sig\_peptide

/\*tag= b 243..1136

195..242 195..1139 /\*tag=

0;

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New nucleic acid encoding Fas protein without its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Fas mediated apoptosis
mRNA was obtd. from human lymphocytes and PCR was used to make CDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCR product was ligated into pBluescript and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
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                                                                                                                                                                                                                            AAX24878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant plasmid was used to transfect E. coli DH5-alpha cells.insert sequence of pBluescript-Fas-delta-TM is given in AAQ93879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2153 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 2212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX24878 standard; DNA; 2471 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.0%; Score 226;
Local Similarity 100.0%; Pred. No..
es 226; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                   Fas receptor; Fas ligand; Fast; proinflammatory; immunosuppressive; graft versus host disease; autoimmune disease; psoriasis; rheumatoid arthritis; systemic lupus erythematosus; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soluble Fas receptor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX24878;
                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                    Mammalia.
                                                                                                                                                                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                           polyA_signal
                                                                                                                                                                                                                                                                                          mat_peptide
                                                                                                                                                                                  28-JAN-1999.
                                                                                                                                                                                                           WO9903999-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                             (UNMI ) UNIV MICHIGAN
                                                                                                                                                             16-JUL-1998;
                                                                                        Chen J, Nabel GJ;
                                                                                                                                      17-JUL-1997;
                             Inhibition of proinflammatory responses - using an agent which
                                                     P-PSDB; AAW98070
                                                                   WPI; 1999-132243/11.
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                           97US-0052829
                                                                                                                                                                98WO-US14771.
                                                                                                                                                                                                                                                                                                                     /*tag= a
/transl_except= (pos:519..521, aa:Gly)
195..242
                                                                                                                                                                                                                                                                                               /*tag= b
243..1136
                                                                                                                                                                                                                                                  /*tag= d
2455..2460
                                                                                                                                                                                                                                                                         /*tag= C
2349..2354
                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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AAQ29959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                response in a cell mixture by administering an immunosuppressive agent which inhibits the proinflammatory activity of Fas ligand (FasL). In some embodiments, FasL is coadministered with the immunosuppressive agent, and the cell mixture comprises or neutrophil cells. The method can be practised in vitro, so vivo or certain vivo. Suitable immunosuppressive agents include antisense or ceptors, ribozymes that inhibit endogenous FasL expression, soluble Fas cereptors, ribozymes that inhibit the endogenous expression of cell endogenous expression of cell endogenous expression of cereptors, ribozymes that inhibit the endogenous expression of cell endogenous expression of transforming growth factor (TGF)-beta, cell endogenous expression of transforming growth factor (TGF)-beta, cell endogenous expression of transforming growth factor (TGF)-beta, cell endogenous expression of cell endogenous expression
                                   polyA_signal
                                                                                                                                                                                mat_peptide
                                                                                                               conflict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local ;
                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                        Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 226;
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         Human cell surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ29959 standard; cDNA to mRNA; 2534 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ29959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2153 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 2212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2093 99cactggcacggaacacaccctgaggccaggccttggctgcccaggcggagctgcctctt 2152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ggcaetggcaeggaacaecectgaggceageeetggetgeeeaggeggagetgeetett 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gacgettetggggagtgagggaageggtttaegagtgaettggetggageeteaggggeg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This present sequence is a DNA clone encoding soluble Fas receptor (see AAW98070). The invention provides a method for inhibiting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
Local Similarity 100.0%; Pred. No. 1.*
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 4B; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modulates FasL stimulation, used for treating graft versus host
/*tag= c
/note= "this residue is not present in pF3"
1831..1836
                                                                                                                                                                /*tag= a
243..1199
                                                                                                       /product= Fas_antigen
1046
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 226; DB 20; Length 2471; Pred. No. 1.4e-50;
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В

В δÃ 밁 δõ DЪ

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Plasmid pF58 contg. human Fas cDNA.
                                 19-FEB-1996 (first entry)
                                                                      AAQ95297;
                                                                                      AAQ95297 standard; cDNA; 2534 BP.
                                                                                                                                                                2213 attgctcaaccaaccatgctgggcatctggaccctcctacctctggt 2258
                                                                                                                                                                                                                    2153 otcocgoggsttggtggacccgotcagtacggagttgggggagctcttcacttcggagg 2212
                                                                                                                                                  181 attyctcaacaaccatyctgggcatctggaccctcctacctctggt 226
                                                                                                                                                                                                                                                                            2093 99cact99cac99aacacaccct9a99cca99ccct99ctgccca99cggagctgcctctt 2152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A cDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The cDNA was ligated to BstXI-cut vector pcEV4 via BstXI linkers. The KT3 cDNA library was used to transfect monkey coscatis which were then suspended in buffer containing murine anti-Pas attibodies. The Fas expressing cells adhered with goat anti-mouse Extrachromosomal DNA was prepared from adhered to the plates. Transform E.coli vM100 cells. A 520bp XhoI-BamHI fragment from a longest cDNA clone was designated pF58 and contains an ORF corresp. Loa 335 amino acid pre-protein and a 319 amino acid mature protein (i.e. human Fas antigen).
                                                                                                                                                                                                    121 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 180
                                                                                                                                                                                                                                                                                                                                    2033 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2092
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                                            61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                    1 gacgettetggggagtgagggaageggtttaegagtgaettggetggageeteaggggeg 60
                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 1 and 2; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monocional antibodies that react with tumour cells expressing Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAR28084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-358914/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Itoh N, Nagata S, Yonehara S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OSAB-) OSAKA BIOSCIENCE INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-1992.
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Similarity 100.0%; Pred. No. ...
Organizative 0; Mismatches
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2352..2357
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2518..2
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                                                                                                                           RESULT 11
                                     XGXA
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Best Local 9
    SX S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pF58; human Fas cDNA; soluble membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of soluble membrane proteins \cdot for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ95297 is the plasmid pr58 which contains the human Fas cDNA. The plasmid was used in the construction of an expression vector for the prodn. of recombinant soluble membrane proteins. The proteins the protein be used in antibody prodn. for the treatment and prevention of can be used in antibody prodn. for the treatment and prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR78606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Pages 15-17; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-202847/27.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                       2093 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2152
                                                                                                                                                                                                                                                                                                                        2033 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2092
                                                                                                                                                                                                                                                                                                                                                                                                                                                   related diseases
                                                                                                                                                                                                                         2153 ctcccgcgggttggtggacccgctcagtacggagttgggggaagctctttcacttcggagg 2212
                                                                                                                                                          AAT16303 standard; cDNA; 2534 BP
                                                                                                                                                                                                           121 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 180
Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
                        hFas coding sequence from plasmid pCEV4/hFas.
                                                  06-SEP-1996
                                                                                                                                                                                                                                                           61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                            1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                                                                                                                                                                                                                                                                                                                Conservative
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195..242
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243..1199
/*tag= c
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                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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AAV32993

RESULT

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YXX PN XXX PD YXX PD XXX PF PR PR XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis; serum; systemic lupus erythematosus; ss.
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                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the coding sequence for the human Fas antigen contained within the plasmid pCEV4/DFas. The soluble Fas antigen is included in the immunoassay kit of the invention. The kit is for the included in the immunoassay kit of the invention. The kit is for the say of soluble Fas antigen and contains an immobilised anti-soluble Fas assay is stendard soluble Fas antigen encoded monoclonal antibody, as well as the standard soluble Fas antigen encoded by this sequence. The assay is simple and has high accuracy, high sensitivity, and is capable of assaying a number of different specimens at the same time. The immunoassay is used on biological samples (such as serum) and is useful for diagnosis of autoimmune diseases such as rheumatoid arthritis or systemic lupus erythematosus (SLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoassay method for soluble Fas antigen in body fluids - for diagnosis of auto:immune diseases such as rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hachiya T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     systemic lupus erythematosus
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                                                                                                                                                                                                                 2033 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2092
                                                                                                                                                2093 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2152
                                                                                 2153 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 2212
                121 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg
181 attgetcaaccaaccatgetgggcatctggaccctcctacctctggt 226
                                                                                                                                61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                 1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
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243..1998
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195..242
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195..1201
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0,

AAV32993 standard; cDNA; 2534 BP

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CC The present sequence represents a Fas cDNA sequence used in the CC depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK) (FasL)-expressing activated Fas-expressing CD8+ T-lymphocyte killer (TK) (FasL)-expressing activated CD4+ cells. It involves contacting this CC immune cell population which would interfere with the CC interaction between Fas and FasL. Therefore, the method is useful for CC is the use of the agent which can reduce depletion of activated CC is the use of the agent in the manufacture of therapeutic compositions. Also claimed CC cell surface receptor Fas and its ligand FasL. By interaction of the CC apoptosis of lymphocytes can be triggered by the interaction of the CC apoptosis of CD8+ TK lymphocytes caused by expression of FasL on activated CD4+ cells. Such FasL-expressing activated CD4 cells useful the result of CD4- FasL-expressing activated CD4+ cells of CD4- cell infection with an immunodeficiency virus (SIV). The claimed prevention of apoptosis may then allow treatment (prophylactic and/or therapeutic) of immunodeficiency compositions activated CD4+ cells in fection of apoptosis may then allow treatment (prophylactic and/or therapeutic) of immunodeficiency crus diseases e.g. AIDS.
                                                                                                                                                                                                                                                                                                                                                                           Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency diseases - by interfering with interaction of Fas with Fas-ligand expressed on activated CD4+ cells, e.g. cells infected with HIV
                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 10; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-456867/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screaton GR, Xu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-1998
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1831..1836
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243..1199
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195..242
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Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

The present sequence was used in the development of novel Fas antigen derivatives, which contain a Fas antigen extracellular region lacking one or more amino acid residues in the region fac the amino-terminal to (but excluding) the 1st cysteine residue

in the region from

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                                     Disclosure; Fig 1-2; 102pp; Japanese.
                                                             Fas antigen derivative containing modified extracellular region - has low antigenicity, promotes apoptosis and is useful in treatment
                                                                                                            P-PSDB; AAW50289.
                                                                                                                  WPI; 1997-558981/51.
                                                                                                                                       Nagata S, Nakamura N;
                                                                                                                                                          (OSAB-) OSAKA BIOSCIENCE INST.
                                                                                                                                                                    (MOCH ) MOCHIDA PHARM CO LTD
                                                                                                                                                                                            02-MAY-1996;
                                                                                                                                                                                                                  01-MAY-1997;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                      Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
                                                                                                                                                                                                                                                                                                                                                                                        apoptosis modulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Fas antigen cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV07002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV07002 standard; cDNA to mRNA; 2534 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226;
                                                                                                                                                                                         96JP-0135760.
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243..1199
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195..1202
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; Pred. No. 1.5e-50;
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AAF68854/c
   Query Match
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The derivatives are effective regulators of apoptosis and can be used (either by administration of the polypeptide, for by the use of the coding DNA in gene therapy) to treat a range of diseases, of the coding DNA in gene therapy) to particular viral diseases e.g. diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of such as hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                             Human; lung cancer; lung tumour; lung tumour protein; gene therapy; lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine; cytostatic; antisense inhibition; ss.
                                                                                                                                                                                                               30-JUN-1999;
15-OCT-1999;
17-DEC-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lung tumour protein related nucleotide sequence SEQ ID NO:796.
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000WO-US18061.
                                                                                                                                                                                                                                                                                                                04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                         06-MAR-2000; 2000US-0519642.
22-MAR-2000; 2000US-0533077.
10-APR-2000; 2000US-0540259.
27-APR-2000; 2000US-0560406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 gacgcttctggggagtcagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
Lung tumor-associated proteins and the nucleic lacids that encode them, useful for preventing, diagnosing and treating lung cancer - \,
                                                                                                                                            05-JUN-2000;
                                             WPI; 2001-071488/08.
                                                                                                                 (CORI-) CORIXA CORP.
                                                                          Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                         Bangur CS,
                                                                          Mannion
                                                                                                                                               2000US-0589184.
                                                                                                                                                                                                                                             99US-0346492.
99US-0419356.
                                                                                                                                                                                                                                99US-0466867
                                                                                                                                                                                                                       99US-0476300
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                                                                                          Lodes MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                            Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>, 1</u>
                                                                                                  Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes immunogenic portions of lung tumour-associated proteins (I) and the nucleic acids (NAs) that encode them. (I) have cytostatic activity and can be used in gene therapy, antisense (I) have cytostatic activity and can be used in gene therapy, antisense inhibition and in vaccines. The NAs and the lung tumour-associated inhibition and in vaccines. The NAs and the prevention, treatment and proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with their inappropriate expression, diagnosis of diseases associated with their inappropriate expression, especially lung cancers. For example, the NAs may be administered to especially lung cancers. For example, the NAs may be administered to that affect the activity of the protein by expressing inactive proteins that affect the activity of the protein by expressing inactive proteins that affect the activity of the protein of (I). Additionally, the or make may be used to represent the patients own production of (I). Additionally, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAS may be used to produce the lung-tumour associated protein, according to standard recombinant DNA methodology. Conversely, antisense NA molecules may be administered to down regulate protein expression by molecules may be administered to down regulate protein expression. The NA binding with the cells own genes and preventing their expression. The NA binding with the cells own genes and preventing their expression. The NA binding with the cells own genes and preventing their expression. The NA since the complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar NA sequences in assays and hence which patients may be in need of treatment for lung samples, and hence which patients may be in need of treatment for lung and in assays to identify modulators (agonists and antagonists) of the and in assays to identify modulators (agonists and antagonists) of the and antagonists to AAB768878 represent human lung tumour protein related AAB76848 to AAB76878 represent human lung tumour protein related and protein sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 415-416; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2435 BP; 620 A; 599 C; 614 G; 601 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2374 TAGATTTACAGAGAAGTTGCAGAGATAGTACAAAGAGTTCCTGTATACCCTTCACC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV20441 standard; DNA; 35100 BP
                                                                                                                                                                                                                                                                                                                                                                                                       Human; oncogene; proto-oncogene; neoplastic disease; anticancer; cancer; antisease oligonucleotide; c-fms; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       676 ttttccttccttcttttacatttttttatttaaatgaacttttcattttcattt 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV20441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             736 taggatttcaaaaaatttgcagagataatacagagaatgcccatataccatcctcc 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human c-fms oncogene.
                                                                                                                                                                                                                                                                                                                        US5734039-A.
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                              31-MAR-1998.
                                                                                                                                                                                   15-SEP-1994;
                                                                                                                                                                                                                                15-SEP-1994;
Anticancer composition comprising two anti-sense oligo:nucleotide(s)
                                            WPI; 1998-229882/20.
                                                                                           Calabretta B,
                                                                                                                                    (UYJE-) UNIV JEFFERSON THOMAS
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                                                                                                  Skorski T;
                                                                                                                                                                                        94US-0306691
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 Mismatches

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pred. No. 2.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 2435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
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Search completed: September 7, 2002, 18:39:36 Job time: 29870 sec
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                                                                       3986 ttotttottttttotatotttttgaga 4012
                                                                                                                       The present sequence represents an oncogene from the present invention. The present invention describes a composition which comprises two cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, C-yes. The second oligonucleotide is specific for a proto-oncogene selected from ras, raf, EGF-1, proto-oncogene selected from myc, jun, c-ets, c-for a nuclear oncogene or c-rel, c-wav, c-ski, c-spi, cyclin Dl, pML/RAR alpha, AMLL/MTGS, The combination of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells.
                                                                                                                                                                                                                                             3806 gaggttgcagtgagctgagatcatgccactgcactccagcctaggcgacagagcaagact 3865
                                                                                         714 acttttcattttggaatagttttagga 740
                                                                                                                                          Sequence 35100 BP; 8474 A; 8597 C; 9682 G; 8347 T; 0 other;
                                                                                                                                                                                                                                                                 534 gaagatccacatatgtgagttgctggcttataattcacactcaagagatactgattttgt 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Column 59-90; 92pp; English.

    targetting cytoplasmic and nuclear oncogene(s)

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C 1 125 100.0 506 10 B659590 C 1 125 100.0 617 9 AV695647 C 2 125 100.0 619 9 AL540709 C 3 125 100.0 619 9 AL540709 C 4 123.4 98.7 599 10 BF569266 C 4 123.4 98.7 793 10 BG1763679 C 5 121.8 87.4 10 10 BG121070 C 6 110.8 88.6 1140 10 BG121070 C 7 109 87.2 359 9 AV692383 C 7 109 87.2 391 9 AA383161 9 62.4 49.9 291 9 AA383161 9 62.4 49.9 291 9 AA383161 37 29.6 850 10 BF745387 C 12 36.6 29.3 392 9 AI393907 C 12 36.6 29.3 392 9 AI393907 C 13 36.6 29.3 426 10 BE910359 C 15 36.6 29.3 427 10 BE910359 C 15 36.6 29.3 437 9 AW299892 C 17 36.6 29.3 437 9 AW299892	pred. No. is the number of results predicted by score greater than or equal to the score of the score and is derived by analysis of the total score summaries  **  Result Ouery No. Score Match Length DB ID  No. Score Match Length DB ID	Database: EST:*  1: em_estba:*  2: em_estin:*  4: em_estin:*  4: em_estou:*  6: em_estou:*  6: em_esto:*  10: gb_est1:*  10: gb_est2:*  11: gb_ts:*  12: gb_gss:*  13: em_gss_hum:*  14: em_gss_hum:*  15: em_gss_pln:*  16: em_gss_vrt:*	Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0  Searched: 13736207 seqs, 6748477542 residues Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000  Post-processing: Minimum Match 100% Listing first 45 summaries	GenCore version 4.5  Copyright (c) 1993 - 2000 Compugen Ltd  OM nucleic - nucleic search, using sw model  Run on: September 7, 2002, 14:51:33; Search ti Run on: September 7, 2002, 14:51:33; Search ti  199.361 Mil  Title: US-09-834-291-2_COPY_1_125  Perfect score: 125 Sequence: 125 Sequence: 125 Jantaccgctgggcaggcgggaagctita
BG03930 190747 AV695647 AV695647 AV695647 AV695647 BF569266 662185634 BF763679 603049567 BG121070 602352793 AV692383 AV692383 AV692383 AV692383 AF76387 601578024 AA383161 EST96716 BE745387 6015798024 AI623104 tu49f10 x AI393907 ty05f09.x BE908413 601503332 BE908413 601503332 AI523874 ty97d02.x AW299892 x854h02.x	spredicted by change printed, score of the result being printed, total score distribution.  AARIES  Description		27472414	.5 compugen Ltd. ; Search time 8462.63 Seconds (without alignments) 199.361 Million cell updates/sec
FEATURES Source	TITLE TOURNAL COMMENT	RESULT 1 BG659530/c LOCUS LOCUS DEFINITION AND ACCESSION KEYWORDS SOURCE ORGANISM FOR THE SERVICE SOURCE AUTHORS REFERENCE AUTHORS TO THE SERVICE SOURCE T	00000000000000000000000000000000000000	c 19 36.6 c 20 36.6 c 21 36.6 c 21 36.6 c 22 36.6 c 22 36.6 c 25 36.6 c 27 36.6 c 28 36.6 c 29 36.6 c 31 36.6

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	AT311654 go91b09.x	RG057357 naf14a02.	AW250964 2822123.3	BF663371 602144324	AGENCOON		60236632	RE798007 601583939	9	ω	3	_	1 AU1446/1	7 10000	100007		AW044313 WV67902.X	AW015515 UI-H-BIOP	AI760624 wi52dl2.x	7 7h88e0	49565 7	5	AW068798 cn25al0.x	3	BG236320 nat26b10.	0	oy75a06	AI982659 wt53e05.x		BG057358 nafl4a03.

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                  Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                 Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                             Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                                                                                                      Contact: Zeguang Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AV695647 GKC Homo sapiens cDNA clone GKCFCD11 5', mRNA sequence.
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                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKCFCD11"
                                          /lab_host-"SOLR"
                                                   /tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
                                                                                          /clone_lib="GKC"
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a small percentage contaminants from human fibroblast
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61 gaggtgggggggggggggacaggaattgaagcggaagtctggggaagctttagggtcgc 120
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Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 899)
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                                                                                                                                                                                                                  /note-"Organ: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime and enriched, double-stranded cDNA was digasted with Not I pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a Maryland 20850, USA Fax: (1) 301 610 8371 Email: http://fillen.k.
                                                                                                                                                                                              http://fulllength.invitrogen.com", 288 c 245 g 170 t
                                                                                                                                                                                                                                                                                                                                                                        /clone="CSODE002YN18"
/clone_lib="LTI_FL002_PL1"
                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
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Clone distribution: MGC clone distribution information can be clone through the I.M.A.G.E. Consortium/LLNL at: found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov column: 10 plate: LLCM1184 row: column: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.go
Tissue Procurement: Linehan
                                             TGGAG 26
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/clone_tib="NIH_MGC_45"
/clone_tib="NIH_MGC_45"
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99.2%; Pred. No. 2.5
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BO3049567F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189752 5',
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1 (bases 1 to 793)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue procurement: Life Technologies, Inc.
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Plate: LLAM11474 row: e column: 17
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Similarity 98.4%; Pred. No. 6.2e-19;
                                                                                                                                         BG121070 1140 bp mRNA linear EST 30-04
602352793F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4451039
                                                         BG121070.1 GI:12614579
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         human.
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/note="organ: pooled colon, kidney, stomach; Vector:
/note="organ: pool of stolens, age 26 yo male, 49 yo
pcMV-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
pcMV-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed), 49 yo
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
female, 71 yo male and 70 yo female. Library is
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV Site is
oligo-dT primed and directionally cloned (EcoRV although Average insert size 1.4 kb,
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full-length clones and was constructed by C.
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Gruber (Invitrogen). Research Genetics tracking code
133 Note: this is a NIH MGC Library."
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/clone_lib="NIH_MGC_116"
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EST 30-JAN-2001

ORGANISM

Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 GAGGTGGGGGTGGGGACAGGAATTGAAGCGGAAGTCCTGGGAAGCTTTAGGGTCG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 GACCCCGCTGGGCAGGCGGGCAGCTCCGGGCGCTCCTCGGAGACCACTGCGCTCCACGTT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                   43 CTGGAG 38
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Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gaggtgggcgtgggggggggacaggaattgaagcggaagt-ctgggaagctttagggtcg 119
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                             AV692383
AV692383 GKC Homo sapiens cDNA clone GKCEWG05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123; Conservative
                                                                                                                                                                                                                                                                                 AV692383.1 GI:10294246
                                                                                                                                                                                                                                                       human.
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High quality sequence stop: 727.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
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/lab.host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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/clone_11b="NIH_MGC_90"
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/db_xref="taxon:9606"
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97.6%; Pred. No. 2.4
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 Mismatches

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                                                                                                                                      Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

http://image.llnl.gov

Plate: LLAM11681 row: j column: 03
                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 800)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              603204413F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5270114 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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                                /clone="IMAGE:5270114"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="organ: testis; Vector: pBluescriptR (modified
                                                                                          /organism="Homo sapiens"
                                                                            /db_xref="taxon:9606"
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/dev_stage="Adult"
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Mammalia; Eutheria; Primates; Catarrihini; Hominidae; Homo.

Romania; Localia; Localia
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AA383161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence based upon 83 million nucleotides of cDNA sequence 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                    Bioinformatics
                                                                                                                  For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi/html)
                                                                                                                                                                                                                                                                                                Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                        Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                      3018699423
                                                                                                                                                                                                                                                                                                                             Medical Center Drive, Rockville, Mp 20850 USA
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98.5%;
/organism="Homo sapiens"
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Pred. No. 2.5e-05;
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BE745387
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   BASE COUNT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Nathymac http://mgc.nci.nih.gov/.
Nathymac http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE745387 850 bp mRNA linear EST 15-SEP-2000 BE745387 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927029 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE745387.1 GI:10159379
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BE745387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: LLCM755 row: p column: 06 High quality sequence stop: 722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM755 row: p column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics information can be Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma"
/tisue_type="adenocarcinom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="ATCC (inhost):187517"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Testis I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:3927029"
/clone_lib="NIH_MGC_9"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.9%;

 Mismatches

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pred. No. 3.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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Local Similarity

64;

Conservative

29.6%; 58.7%;

Score 37; pB 10; Length 850; pred. No. 35;

Mismatches

45;

Indels

0; Gaps

0;

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BASE COUNT
ORIGIN
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                                                                                                                                                                         Query Match
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                                             225 Trécacegééergaaceacadegegegerecegraagacerecegacececegerege 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
63 99t999c9t999999c9gacaggaattgaagcggaagtctgggaagc 109
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                                                                       3 tecegetgggeaggegggeageteeggegeteetegggagaecaetgegeteeaegttga 62
                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 GGGGTGGGGGGGTGTCCGTCCGGAAATGAAGGAATAGCCCCGAGGACC 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 GCTTCCACCGGGCCTGAACCACAGCGGAGGAGCTCCGCTAAGACCTCCCCCACCCCCGCTG 520
                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gatcccgctgggcaggcggggcagctcccggcgctcctcggagaccactgcgctccacgtt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

Insert Length: 397 Std Error: 0.00

Seg primer: 40Up from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 321 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                   Conservative
                                                                                                                                                                                                                                           78
                                                                                                                                                                                                              /Note-"Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; plasmid DNA from the circles were made in vitro. Following HAP purification, reaction. The driver was PCR-amplified cDNAs from a pool 98508-986759, 1101192-1101959, and 1117928-1220615).

Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:2254411"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                29.38;
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                                                                                                                                   0,
                                                                                                                                            Score 36.6; DB 9;
Pred. No. 37;
                                                                                                                    Mismatches 44; Indels
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                                                                                                                                                   Length 333;
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ACCESSION
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AI393907/c
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                                                                                                                 171 GGTGGGGGGGGTGTCCGGTCCGGAAATGAAGGAATAGCCCGAGGACC 125
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                                                                                                                                                                             231 TTČĆAČCĞĞĞCTĞAACCAČAĞCĞGAĞĞAĞĞTČCĞCTAAĞACĞTĞCCCACCCCGCTĞĞĞ 172
                                                                                                                                     3 tecegetgggeaggegggggeageteeteggeggagaecaactgegeteeacgttga 62
                                                                                                                                                                                                                                                                                      Local Similarity
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BE908413 426 bp mRNA IHEAL ESTATOR 601503040F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905120 5',
                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Allzadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing Center found through the I.M.A.G.E. Consortium/LLNL at:
Insert Length: 746 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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### tg05f09.xl NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107913 3',
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                                                                                                                                                                                                                                                                                                                                                                       92 a
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                                                                                                                                                                                                                                                                                                                                                   T 3/j; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
Library is normalized, and was constructed by Bento
soares and M.Fatima Bonaldo."

128 c 101 g 71 t
                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:2107913"
/clone_1ib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                29.38;
58.98;

 Mismatches

                                                                                                                                                                                                                                                                             Score 36.6;
Pred. No. 38;
                                                                                                                                                                                                                                                                                    DB 9; Length 392;
                                                                                                                                                                                                                                                       44; Indels
                              EST 20-OCT-2000
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VERSION
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TITLE
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BE910359
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                                                                                                                                                            TITLE
                                                                                                                                                                             AUTHORS
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9711 row: o column: 09 High quality sequence stop: 420. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BE910359
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                                                                                                                                                                                                                                                                                                                      BE910359.1 GI:10406871
                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                          Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) bnA Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can be
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/lab_host="Upine" (phage-resistant)"
/note="Organ: pancreas; vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: pancreas; vector: pCMV-SPORT6; Site_1: Oligo dT.
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
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plate: LLAM9711 row: p column: 07
High quality sequence stop: 426.
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cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome information can be
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consorthum/LLNL at:

www-bio.llnl.gov/bbr/jimage/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
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/tissue_type="epithelloid carcinoma"
/lab_host="0H10B (phage=resistant)"
/note="Organ: pancreas; Vector: pCMV-SpoRT6; Site_1: NotI;
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/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
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Search completed: September 7, 2002, 14:51:36 Job time: 16195 sec

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                                                  pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Query
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1 (bases 1 to 266)

1 (bases 1 to 266)

Mueller-Schilling,M., Krammer,P. and Oren,M.

Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy patent: DE 1944779-C 32 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE)
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Sequence 32 from Patent DE19847779.
AX026120
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J. Exp. Med. 188 (11), 2033-2045 (1998)
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Mueller,M., Wilder,S., Bannasch,D., Israeli,D., Lehlbach,K.,
Li-Weber,M., Friedman,S.L., Galle,P.R., Stremmel,W., Oren,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-SEP-1998) Mueller M., Department of Internal Medicine IV, University Hospital, Bergheimerstr. 58, Heidelberg, 69115,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens DNA for enhancer of CD95 gene, partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muschen,M., Re,D., Brauninger,A., Wolf,J., Hansmann,M.L., Diehl,V., Kuppers,R. and Rajewsky,K.
Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction
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/db_xref="GI:13539241"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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h 100.0%; pred. No. 1.1e-18;
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Similarity 0; Mismatches 0;
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Mueller-Schilling, M.; Krammer, P. and Oren, M.

Nuvel receptor dna useful for identifying apoptosis-modulating novel receptor dna useful for cancer chemotherapy substances potentially useful for cancer chemotherapy substances potentially useful for cancer chemotherapy patent; DE 19847779-C 103-FEB-2000; Patent; DE 19847779-C 103-FEB-2000;
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100.0%; Score 125; DB 6; Length 3212; Query Match 100.0%; Pred. No. 8.4e-19; Best Local Similarity 100.0%; Pred. No. 8.4e-19; Indels 0; Matches 125; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          702 bp DNA linear PRI 02-APR-2001
HSA279011
Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo· Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo· Losses 1 to 702)

1 (bases 1 to 702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apo-1 Fas; CD95 antigen; CD95 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuppers,R. tations of the CD95 gene in human B cells as a somatic mutations of the CD95 gene in human B cells as a side effect of the germinal center reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 702) Brauninger, A., Wolf, J., Hansmann, M.L., Diehl, V., Muschen, M., Re, D., Brauninger, A., Wolf, J., Hansmann, M.L., Diehl, V., Muschen, M., and Rajewsky, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (19-SEP-2000) Muschen M., Department of Immunology, 50931 Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                           Related sequences: D31968 X89101 AJ279012 AJ279013.
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                                                                                                                                                                                                                             /gene="CD95"
<1. 313
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                        /cell_type="Reed-Sternberg cells"
/note="Hodgkin's disease tissue"
                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
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                                                                                                                                     /standard_name="Apo-1 Fas"
                                                                                                       /gene="CD95"
/translation="MLGIWTLLPLV"
314. >702
                                                                                        /standard_name="Apo-1 Fas"
                             /protein_id="CAC35539.1"
/db_xref="GI:13539239"
                                                            /product="CD95 antigen"
                                                                            /codon_start=
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/gene="CD95"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           615 GAGGTGGGCGTGGGGGGGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Related sequences: D31968 x89101 AJ279011 AJ279012.
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                                                                                                                                                                                                 Direct Submission
Submitted (19-SEP-2000) Muschen M., Department of Immunology,
Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gatcccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgtt 60
                                                                                                                                                                                                                                                                    Muschen, M.
                                                                                                                                                                                                                                                                            Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
                                                                                                                                                                                                                                                                                    (bases 1 to 702)

Muschen, M., Re.D., Brauninger, A., Wolf, J., Hansmann, M.L., Diehl, V., Kuppers, R. and Rajewsky, K.
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Catarrhini; Hominidae; Homo.
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Apo-1 Fas; CD95 antigen; CD95 gene.
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HOMO sapiens partial CD95 9gne for CD95 antigen (Apo-1 Fas), exon
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/standard_name="Apo-1 Fas"
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282. .>313
                    /gene="CD95"
                                                  /gene="CD95"
                                                                         /standard_name="Apo-1 Fas"
                                                                                            /gene="CD95"
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/note="Hodgkin's disease tissue-polymorphic allele (+337)"
                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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99.28;
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COMMENT
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Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Cione requests: clonerequest@sanger.ac.uk crows control of this sequence version replaced gi:14161146. Together with a note of the overlapping clone name. Note that the where differences are found thas are annotated as variations corresponding to the overlapping clone, as we submit sequence with a note of the overlapping clone name. Note that the rail as sequence was finished as follows unless otherwise noted: all as compressions were either double-stranded or sequenced with an alternate one plasmid subclone or more than one will sequence with an alternate one plasmid subclone or more than one will sequencing problems, such abbreviations are used to associate primary accession numbers given the feature table with their source databases: Em; EMBL; Swisspror. Tr.; TREMBL, Wp: was generated from part of bacterial clone contigs of human http://www.sanger.ac.uk/Projects/C-elegans/wormpep This sequence http://www.sanger.ac.uk/Eprojects/C-elegans/wormpep This sequence http://www.sanger.ac.uk/Epro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL157394
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product="cD95 antigen"

protein_id="0Ac35541.1"

/db_xref="G1:1539243"
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Pred. No. 5.7e-18;
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protein_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.chori.org/bacpac/home.htm
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similarity 98.4%; pred. No. 2.2e-18;
Similarity 98.4%; pred. No. 2.2e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                             D31968.1 GI:961455
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens blood DNA, clone pF7.
                                                                                                                                                                                                                                            Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection j. Biol. Chem. 270 (30), 18007-18012 (1995)
                                                                                                                                                                                                                                                                                                             Wada,N., Matsumura,M., Ohba,Y., Kobayashi,N., Takizawa,T. and
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2165)
                                                                                                               Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Faculty of Pharmaceutical (E-mail:nakanaka@dbs.p.kanazawa-u.ac.jp, Ishikawa 920-0934, Japan (E-mail:nakanaka@dbs.p.kanazawa-u.ac.jp, Tel:076-334-4424, Fax:076-234-4480)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Sequence from AC015461 sequenced by WIBR." 105973. .105989 /note="Sequence confirmed by AC015461 sequenced by WIBR." a 36398 c 36888 g 58358 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-11.2"
100119. 100156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Sequence from AC015461 sequenced by WIBR." 105808. 105972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Sequence confirmed by AC015461 sequenced by WIBR."
         /tissue_type="blood" 79. .87
                                         /clone="pF7'
                                                       /db_xref="taxon:9606"
                                                                      /organism="Homo sapiens"
                                                                                                     ocation/Qualifiers

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2165 bp
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ORIGIN
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AF272328
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                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gatcccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgtt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                          misc_RNA
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AF2
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                                                                                                                                                                                                                                                                                                                                                                                                          Chanderball, A.S., van der Werff, H. and Renner, S.S. evidence from phylogeny and historical biogeography of Lauraceae: evidence from phylogeny and historical biogeography
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF272328.1 GI:14090803
                                                                                                                                                                                                                                                                                                2 (bases 1 to 733)
Chanderball, A.S., van der Werff, H. and Renner, S.S.
                                                                                                                                                                                                                                                                                                                                                        the chloroplast and nuclear genomes Ann. Mo. Bot. Gard. 88 (1), 104-134 (2001)
                                                                                                                                                                                                                   Submitted (26-MAY-2000) Biology, University of Missouri-St. Louis, St. Louis, Missouri 63121, USA 8001 Natural Bridge Rd., St. Louis, Missouri 63121, USA
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481. .489
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276. .:
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1814. >2165
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/protein_id="BAA20850.1"
/db_xref="GI:4433150"
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555 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.5%; Score 109.4; DB 9; Length 2165; 99.1%; Pred. No. 2.9e-15; 99.1%; Pred. No. 2.9e-15;
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spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 26S ribosomal RNA*
                                                       /note="contains 18S ribosomal RNA, internal transcribed
                                                                                                            /db_xref="taxon:128687"
                                                                                                                                           /organism="Phoebe formosana"
                                                                                                                                                                                             Location/Qualifiers
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BASE COUNT

138 a

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DEFINITION Sequence 2726 from Patent W00194629
                                              AX332217
                                                             RESULT
                                     LOCUS
                                                                                                                                                                                                                                                                  ORIGIN
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                                                                                                                                                                                                                          Query Match
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                                                                     934 GGTGGGGGGGGGTGTCCGTCCGGAAATGAAGGAATAGCCCGAGGACC 980
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                                                                                                                 874 TTCCACCGGGCCTGAACCACAGGGGAGGAGCTCCGGCTAAGACCTCCCCACCCCCGGTGGG 933
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                                                                                      63 ggtgggcgtggggggggacaggaattgaagcggaagtctgggaagc 109
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                                                                                                                                       3 tecegetgggeaggeggggeageteeggegeteeteggagaceaetgegeteeaegttga 62
                                                                                                                                                                                                         Local Similarity
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                            AX332217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 9aggtgggggggggggggacaggaattgaagcggaa 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 GAGCGCGCCCCGGGGGGGGGGGGGGGGGGGGGGTYCCCGCGAGCTKCGAACMACAAC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y Match

29.4%; Score 36.8; DB 8; Length 7:
Local Similarity 54.1%; Pred. No. 75;
hes 53; Conservative 9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gatcccgctgggcaggcggggcagctcccggcgctcctcggagaccactgcgctccacgtt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolation of a cDNA which corrects chromosome breakage in Fanconi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens cDNA to mRNA.
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                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                          1245.
377 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA repair protein mRNA, complete cds.
                                                                                                                                                                                                                                                                            /product "DNA repair protein"
/product "DNA repair protein"
/protein_id="AAA50503.1"
/db xref="GI:495861"
/translation="MpLUGLOPORSSQAPWSCSPPRGLPSDYGRPLSFPPPRIRESIQ
EDIAEEAPCLOGGRASGLGEAGMSAWLRAIGLERYEEGLVHNGWDDLEFLSDITEEDL
                                                                                                                                                                                                                                                                                                                                                                         /Standard_name="51C protein"
/function="corrects chromosome breakage in Fanconi anemia
                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="immortalized fibroblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         xref="taxon:9606"
l_line="GM 639"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA repair protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 c
                                                                                                                                                                                                                                                                                                                                                                                                                 (vector pbluescript) (vector lambdaYES)"
                                                                                                                                                                                         0;
                                                                                                                                                                         Score 36.6; DB 9; Length 1 Pred. No. 76; Length 1 O; Mismatches 44; Indels
                                                                                                                                                                                                                                                              413 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1269 bp
                                                                                                                                                                                                                                                             263 t
           DNA
                                                                                                                                                                                                _ DB 9; Length 1269;
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           linear
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PAT 09-JAN-2002
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В

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FEATURES
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HUM51C
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4262 TTCCACCGGGCCTGAACCACÁGCGGAGGAGCTCCGCTAAGACCTCCCCACCCCGCTGGG 4321
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                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4657)
Hejna,J.A., Saito,H., Merkens,L.S., Tittle,T.V., Jakobs,P.M., Whitney,M.A., Grompe,M., Friedberg,A.S. and Moses,R.E. Cloning and characterization of a human cDNA (INPPL1) sharing Genomics 29 (1), 285-287 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51C protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human (clone 51C-3) 51C Protein mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUM51C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avalon Pharmaceuticals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AX332217.1 GI:18122851
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GRLVLLRRQRDSQEDWTTFTHDRIRQLIKSQRVQNKLGVVFEKEKDRTQRKDFIFVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                        /clone="51C-3"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:556191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO 0194629-A 2726 13-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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1394 c 1392 g 91.
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1. .4657
                                                                                                                                                                                                                                  _line="GM 639"
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polyA_signal
BASE COUNT 9
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4322 GGTGGGGGCGGGTGTCCGGGAAATGAAGGAATAGCCCGAGGACC 4368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4262 TICCACCGGGCTGAACCACAGCGGGAGCTCCGCTAAGACCTCCCCACCCCCGCTGGG 4321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 ggtgggcgtgggggggggacaggaattgaagcggaagtctgggaagc 109
                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pesesse, X., Deleu, S., De Smedt, F., Drayer, L. and Erneux, C. Identification of a second SH2-domain-containing protein closely related to the phosphatidylinositol polyphosphate 5-phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens mRNA for inositol polyphosphate 5-phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-JUL-1997) X. Pesesse, Interdisciplinary Research Institute, Universite Libre de Bruxelles, Campus Erasme Bldg. (808 Route de Lennik, 1070 Brussels, BELGIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inositol polyphosphate 5-phosphatase; SHIP2 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98042455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 239 (3), 697-700 (1997)
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PRPPLPPGFSATKNAIT
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EVTVTIPHDIYVFGTOENSVGDREWLDLLRGGLKELTDLDVRPIAMOSLWNIKVAVLV
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NONYLDILRLISIGDROLNAFDISLRFTHLFWFGDLNYRLDMDIQEILNYISKKEFEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:2653423
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                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Pred. No. 61;
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Matches

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AP000593 LOCUS RESULT

SOURCE

REFERENCE

FEATURES COMMENT

/clone="CMB9-4J8"

KEYWORDS VERSION ACCESSION ő 밁

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RESULT

Locus

SOURCE

VERSION

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DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
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                                                                                                                             and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                  Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                  AP000593.4 GI:17425220
                                                                                                                                                                                                             Submitted (12-OCT-1999) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Pr
1 (bases 1 to 124635)
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LGKTLDEVTVTIPHDIYVFGTQENSVGDREWLDLLRGGLKELTDLDYRPIAMOSLWNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVDVEGGRLVLLRRQRDSQEDWTTFTHDRIRQLIKSQRVQNKLGVVFEKEKDRTQRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPKAHPRPPLPPGPSPASTFLGEVGSGDDRSCSVLQMAKTLSEVDYAPAGPARSALL
PGPLELQPPRGLPSDYGRPLSFPPPRIRESIQEDLAEEAPCLQGGRASGLGEAGMSAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="encodes 5-phosphatase catalytic domain"
1 1466 c 1448 g 890 t
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1491. .2428
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Pred. No. 60;
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ORIGIN BASE COUNT

BASE COUNT 31089 a 29103 c 30489 g 33954 t

Query Match

29.3%; Score 36.6; DB 9; Length 124635;

Best Local Similarity 58.9%; Pred. No. 34;

Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps

Ov 3 toccorrections

Search completed: September 7, 2002, 18:26:54

AX026091 AX026091 AL157394

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OM nucleic - nucleic search, using sw model
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perfect score:
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 compugen Ltd.
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                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Ice Mammalia; Eutheria; Primates; Catarrhini; Homo.

Mammalia; Eutheria; Primates; Primates; Mopptosis-modulating

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Mueller-Schilling, M., Krammer, P. and Orén, M. M. Willer-Schilling, M., Krammer, P. and Orén, M. M. Weller-Schilling, M. Geful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 3 03-FEB-2000; Patent: DE 1984779-C 3 03-FEB-2000; Patent: DE 1984779-C 3 03-FEB-2000;
                                                                                                                                                AX026091 2380 bp
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/organism="Homo sapiens"
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                    721 AATACTGAAACCTTTAGTGTGTCCCAGTCTGGAACTGCATCCAAATTCAGGTTCAGTAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                      corresponding to the overlapping clone, as we submit sequences with rhis sequence was finished as follows unless otherwise noted: all sequence was finished as follows unless otherwise noted: all chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest. The following in the feature table with their source databases: Em: EMBL; Sw:, database can be found at his providence of the covered by at least subclones are used to associate primary accession numbers given feature table with their source databases: Em: EMBL; Sw:, database can be found at his providence of the more than one the wormper and the hit is succession on the wormper succession on the wormper succession on the wormper succession on the wormper database can be found at his providence of the worm of the wormper military accession on the wormper succession succession on the wormper succession on the wormper succession succession on the wormper succession successio
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This sequence is the entire insert of clone RP11-399019 The true left end of clone RP11-496H23 is at 166408 in this sequence. The true right end of clone RP11-304I5 is at 18704 in this sequence.
                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 of Pieter de Jong. For further details see
                                                                                                                                                                                         http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       requests: clonerequest@sanger.ac.uk
On Aug 31, 2001 this sequence version replaced gi:14161146.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Human DNA sequence from clone RPI1-399019 on chromosome 10,
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malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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              301 gaacttgaggataattagacgtacgtgggtagagggtagggggaagggggtatggcataga 360
301 GAACTTGAGGATAATTAGACGTACGTGGGTAGAGGGTAAGGGGGAAGGGGGTATGGCATAGA 360
                                                    241 CTAAGATTATTTGACCATGAAACATATGTCTCCCCACAAAGCACATATTCCCTATCTCCTT 300
                                                                 241 ctaagattatttgaccatgaaacatatgtctccccacaaagcacatattcctatctcctt 300
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Local Similarity 87.0%; Pred. No. 0;
Docal Similarity 87.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mueller-Schilling, M., Krammer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 1 03-FEB-2000;
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1 (bases ] to 3212)
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/db_xref="taxon:9606"
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                                                                   Submitted (26-MAY 1995) F.H. Rudert, Genesis Research & Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND
                                                                     Development, Corporation Ltd., PO Box
Overlaps with x81335, 6 x82279 x82286.
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                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                  Rudert,F., Visser,E., Forbes,L., Lindridge,E., Wang,Y. and
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717. .801
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/map="q24.1"
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AUTHORS TITLE JOURNAL MEDLINE

Rudert, F.H.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection J. Biol. Chem. 270 (30), 18007-18012 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wada, N., Matsumura, M., Ohba, Y., Kobayashi, N., Takizawa, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2165)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Faculty of Pharmaceutical Sciences; 13-1
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                                                                                                                                                                            481 GGTGGTAAGTGCAGTGACAGATGCAAAACACAGGGTGATGGAAAGCCCCTCAGGAGGGTAA 540
                                                                                                                                                                                      927 ggtggtaagtgcagtgacagatgcaaaacacagggtgatggaaagccctcaggagggtaa 986
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1877)
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                                                                 APO-1 gene; apt gene.
                                                                                                  H.sapiens APT gene, exon X81335
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                                                                                 X81335.1 GI:537410
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exon		REFERENCE
	Behrmann, I., Waltzan, F. www. Structure of the human APO-1 gene Structure of the human APO-1 3057-3062 (1994)	
mRNA	TO TOTAL H AND Krammer, P.H.	

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| 1107 taattgggaagggagagggttgcagagtgaggtgcagagcttggtggacgatgccaaag 1166
                                                                                                     480 GGTGGTAAGTGCAGTGACAGATGCAAAAACACAGGGTGATGGAAAGGCCCTCAGGAGGGTAA 539
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660 TAATTGGGAAGGGAGAGAGGTTGCAGAGTTGAGGTGCAGAGCTTTGGTGGACGATGCCAAAG 719
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X81338.1:145. .253,X81339.1:552. .613,X81339.1:766. .828,
X81340.1:79. .161,X81341.1:235. .279,X81342.1:103. .>1757)
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HSFASX1
LOCUS
DEFINITION H.sapiens Fas, Apo-1 gene (promoter and exon I).
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                                                                                                                                        1620 AGTGACTTGGCTGGAGCCTCAGGGGGGGGGGGACTGGCACGGGAACACACCCTGAGGCCAGCC
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1247 ccttctgtaaaattcatgctaaactacctaagagctatctaccgttccaaagcaatagtg 1306
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Cheng, J., Liu, C., Koopman, W.J. and Mountz, J.D.
Characterization of human Fas gene. Exon/intron organization and
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                                                                              Sequence 2392 from Patent WO0200928.
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                                                 1487 gggccctcccttttcagagccctatggcgcaacatctgtactttttcatatggttaactg 1546
942 PACTATACGATTTAACTTAATTAACTTATTTTCCTCTTAAAAAATAAAAACTAAA 883
                                       882 AAACCCTTTTTCAAAACCCTATAACGCAACATCTATACTTTTTCATATAATTAACTA 823
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Diagnosis of diseases associated with the immune system
Fridance ac (nr.)
Fridance ac (nr.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           702 AACAAAACCTCTACGCTCTAAACTCCATTCTCCTTCAAAACCTCCCCAACTTCCCAAATT 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              762 AAATACCCCCCCAAATCTTTCTCTAAATAACTCCAACAATTAACCAAAACTCCTATACCCA 703
                                                                                                                                                                                                artificial sequence.
                                                                                                                                                                                                               synthetic construct.
                                                                                                                                                                                                                                      AX347320.1 GI:18495208
                                                                                                                                                                                                                                                    Sequence 2391 from Patent W00200928.
                                                                                                                                                                                                                                                                       AX347320
                                                     Conservative
                                                                                                              398 a
                                                                                       /organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
a 51 c 423 g 736 t
                                                                                                                                          Location/Qualifiers
1. .1608
                                   30.3%; Score 856.8; DB 6; Length 1608;
76.7%; Pred. No. 2.2e-206;
ative 0; Mismatches 322; Indels 1; Gaps
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Mon sep 9 09:30:39 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1218 GTTTTCGTGAGTTTTTGATTTCGCGTAAGAGTGATATATAGAGGTGTTTAAAGACGT 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
DEFINITION
ACCESSION
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1278 TTTTGGGAGTGAGGGAAGCGGTTTACGAGTGAGTTTGGAAGTTTTAAGGGGGCGGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2099 tegenegaacacocctgaggccagccctggctgcccaggcggagctgcctcttctccc 2158
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                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                      NISM Homo sapiens thereia; Chordata; Craniata; Vertebrata; Homo.

Bukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.

Likaryota; Butheria; Primates; And Oren, M.

Lobase; Lo 720), Krammer, P. and Oren, M.

Lobase; Lilling, M. useful for cancer chemotherapy

LC 1. (Dases Lilling, M. useful for cancer chemotherapy

Novel receptentially 203-FEB-2000;

Substr. DE 1984779-( DE)

Substr. DE 1984779-( DE)

Locatton/Qualifiers

Locatton/Qualifiers

1. 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720 bp. 720 bp. 720 sequence 2 from Patent DE19847779.
                                                                                                                                                                                                                                  2213 aagoettagggteggaggggaectootggacaa 2272
                                                                                                                                                                          165
                                                                                                                              2393 gogggggagagoctgcagcotcagaacagatattgctcatttctggcagtt 285
                                                                                                 2393 ctcagacgtaggaaataagtcagcacégaagcagtggttaagccggaagggctcggaagaa 2452
                                                      2453 oggoacetttottotogaaaagttatatgggggotgaatgagottotggaggcttgt 2512
                                                                                       286 CTCAGACGTAGGAAATAAGTCAGCACGGAAGCAGTGGTTAAGCCGGAAGGCTCGGAAGAA 345
.../20m-"Homo sapien's"
/organism-"taxon:9606" | 181
/db-xref-"taxon:216 g | 181 c
                                                                                                                                                                                                                                                                                    21.6%: Score 6.1.8; DB 6; Length 720; 21.6%: DB 6; Length 720; DB 6; Length 720; DB 6; Length 720; DB 6; Length 720; DB 6; Length 72
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G27038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2753 aaacttgagcagcctgttttgaaaagtccctcgctcagaaatgccagcttgcagatggct 2812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
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SHGC-30
G27038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                 contact: Michael Olivier, David R. Cox
contact: Michael Olivier, David R. Cox
stanford Human Genome Center Medicine CA 94025, USA
stanford University School Palo Alto, CA 94025, USA
stanford University School Palo Alto, CA 94025, USA
stanford University School Palo Alto, CA 94025, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2
11near STS 30-MAR-2
398 bp DNA 1. Inear tagged site.
38008 Human Homo sapiens STS genomic, sequence tagged
                                                                                                                                                                                                                                                                                                  protocol
                                                                                                                                                                                                                      Buffer:
                                                                                                                 prepared with primer pairs provided by Sandoz, derived from H86126
prepared with primer pairs provided by Sandoz, derived from H86126
prepared with primer pairs provided by Sandoz, derived from H86126
                                                                                                                                                                                                                                                                                                                                                                                   Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                              polymerization:
pCR Cycles:
                                                                                                                                                                                                                                                                                                                                                              penaturation:
                                                                                                                                                                                                                                                  rad polymerase: (
rotal vol:
                                                                                                                                                                                                                                                                                                                   Thermal Cycler:
                                                                                                                                                                                                                                                                                               Template:
                                                                                                                                                                                                                                                                      each 200 uM
0.05 units/ul
10 ul
                                                                                                                                                                                                                                                                                                                                                    94 degrees C for 15 seconds
62 degrees C for 30 seconds
72 degrees C for 30 seconds
                                                                                                                                                                                                        2.5 mM
50 mM
20 mM
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REMARK
COMMENT
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AUTHORS
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                        ORGANISM Homo sapiens
                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                            DEFINITION
Clone distribution; MGC clone distribution information can be found the r.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                           Contact: http://www.ngsc.bcm.tmc.edu/cdna/
Villalon,D.K. Juna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
Muzny,D.M., Gibbs,R.A. Holdson, A., Bouck, J., Yu, W.,
                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                     Email: College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                   2793 atgocagottgoa-gatggotaatcaaagag 2822
                                                                                                                                             Direct Submission
Submitted (15-AUG-2001) Mational Institutes of Health, Mammalian
Institute, 31 Center Drive, Room 11A03. Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                            241 ATGCCAGCTTGCAGGATGGCTAATCAAAGAG 271
                                                                                                                                                                                                                                                                                                                                                         2733 99c9cctattattg9ccaagaaacttgagcagcctgttttgaaaagtccctcgctcagaa 2792
                                                                                                                                                                                                                                                                                                                                                181 GCGCCTATTATTGGCCAAGAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAA 240
                                                                                                                                                                                                                                                                                                                                                                                        2673 gtgatttetgottggtotoctgottggggttggtggtagtcgtteccaccgcacagaaccc 2732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 9.2%; Score 259; DB 11;
Matches 270; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                            121 GTGATTTCTGCTTGGTCTTGCTGCTGGGGTGGGTGGTGCTACTCCTTCCCACCGCACAGAACCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer_bind
BASE Primer_bind
ORIGIN
                                                                                                                                                                                                                                                          Homo 2479
Homo Sapiens, Similar to 2719 bp
superfamily, Member 6, clumor necrosis factor receptor
Homo 3470 cds. Member 6, clone MGC:21432 IMAGE:4514272, MRNA,
RC013470 cds. MRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2553 gtetecettecegggaattetetetetteaagaetgtaagtegetgeetgagtegetgagtegetgetteattt 2612
                                                                                                                                                                                     Taryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                              BC012479
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GTCTCCCTTCCGGGAATTCTCTCTTTAAACACTGTAAGTCGCTGCCCTGAGTGGTTTCAATTT 60
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93 C 105 9 125 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Organism="Homo sapiens"
/Map="10" taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <sup>us-09-834-291-4.rg</sup>e
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REFERENCE
AUTHORS
                                            JOURNAL
                                                             TITLE
                                                                                                                     KEYWORDS
SOURCE
                                                                                                                                  ACCESSION
VERSION
                                                                                                       ORGANISM
                                                                                                                                                                     RESULT 14
HSA279011
                                                                                                                                                      DEFINITION
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                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                          B
Eukaryota....

Mammalla; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Vertebrata; Euteleostomi; Kuppers, M., Re, D., Jungnickel, B., Diehl, V., Rajewsky, Homo.

Side effect of the germinal center reaction B cells as a
                                                                                                                                                                                                           2158 cgcgg 2162
                                                                                                                                                                                    2098 ctggcacggaacacacctgaggccaggcctggctgcccaggcggagctgccttctcc 2157
                                                                                                                                                                            2038 cttctggggagtgagggaagcggtttacgagtgacttggctggagcctcagggggca 2097
                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
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Best Local Similarity 8.7%; Score 245; DB 9; Length 271.

O; Mismatches 0; Indels
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                 1978 ggcttttcgtgagctcgtctctgatctcgcgcaagagtgacacaggtgtcaaagagcg 2037
                                                                                                                                                                                                                                                                      61 GCCTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACG 120
                                                                                           HSA279011
HOmo sapiens Partial CD95<sup>702</sup> bp DNA
1 linear PRI 02-APR-2001
EXON EXOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                       011.1 G1:13539238
Fas: CD95 antigen; CD95 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Source
                                                                                                                                                                                                                                                                                                                                                                                               904 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Series: IRAK Plate: 28 Row: i Column. A passed the following selected for full length sequencing selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                             /Codon_start=1
/product="Similar to tumor necrosis factor receptor
/brotan_d="AHIZA79,1"
/brotan_d="AHIZA79,1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone=MGC.21432 TWAGE:4514272 Clone_type="Bladder, transitional cell papilloma." Clone_tib="NIH_MGC_93" transitional cell papilloma." Coll papilloma.
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## us-09-834-291-4.rge

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SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                           ""GI:13539241"
"GI:13539241"
"tion="MIGIWTLLPLY"
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens"

13x0n:9606"

"Reed-Sternberg cells"

"Reed-Sternberg tissue-polymorphic allele (+275)"
(in's disease tissue-polymorphic allele (+275)"
                              cotcotgaccaccggggcttttcgtgagctcgtctctgatctcg 2006
                                                                                                                                7.6%; Score 216; DB 9; Length 702;
00.0%; Pred. No. 8.8e-44; Indels
ve 0; Mismatches
1968 x89101 AJ279011 AJ279013.
Lifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD95 gene in human B cells as a
                                                                                                                                                                                                                                                                                                                           ame="Apo-1 Fas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ckel,B., Diehl,V., Rajewsky,K. and
                                                                                                                                                                                                                                                                                           name="Apo-1 Fas"
                                                                                                                                                                                                                                                                  _name="Apo-1 Fas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inger,A., Wolf,J., Hansmann,M.L., Diehl,V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Muschen M., Department of Immunology, 50931
LFI E4 R705, Joseph-Stelzmann-Str. 9,
                                                                                                                                                                                                  1_name="Apo-1 Fas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD95 gene in Hodgkin- and Reed-Sternberg
                                                                                                                                                                                     264 9 134 t
                                                                                                                                                      0; Gaps
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Search completed: September 7, 2002, 18:35:34

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OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                        Result
                                           00000
                                                                                                                                                                                                                                                                                                                                                                    pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
18
19
20
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                                                                                                                                                                                                                                                                                                                  Score
                               Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/
2: /cgn2_6/ptodata/2/
3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
5: /cgn2_6/ptodata/2/
6: /cgn2_6/ptodata/2/
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2827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTITY_NUC Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383533 seqs, 122816752 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                  Match Length DB
   /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/SECOMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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     US-08-219-2378-1
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US-08-28-560C-1
US-08-232-463-14
US-08-232-463-14
US-08-232-463-14
US-08-36-0228-10
US-08-36-0228-10
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US-08-306-6918-19
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2 US-08-32-7668-8
2 US-08-32-7668-8
3 US-08-483-942-7
4 US-09-348-942-7
4 US-09-348-942-7
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5 US-08-488-713-5578-35
1 US-08-483-553-24
1 US-08-483-553-24
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US-08-444-231-18
US-08-152-443A-18
US-08-219-237B-1
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                                                                                                                                                                                                           Sequence 1, Appli
sequence 18, Appli
sequence 18, Appli
sequence 1, Appli
sequence 1, Appli
sequence 14, Appl
sequence 14, Appl
sequence 14, Appl
sequence 14, Appl
sequence 10, Appl
sequence 10, Appl
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sequence 2, Appli
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sequence 19, Appli
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sequence 19, Appl
sequence 18, Appl
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RESULT 2 US-08-444-231-18

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APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: 1SPH-0351
                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (221)...(1228)
LOCATION: (221)...(1228)
LOCATION: IMPORMATION:
PUBLICATION: IMPORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 267
VOLUME: 267
LOSUE: 15709-10715
PAGES: 10709-10715
PAGES: 1902-05-25
DATB.1992-05-25
DATBAASE ACCESSION NUMBER: X63717/Genbank
DATBAASE ENTRY DATE: 1996-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEO ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 1, Application US/09290640 Patent No. 6204055
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Best Local S
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                    2128 tggctgcccaggcggagctgcctcttctcccgcgg 2162
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                                                                             gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 120
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tggctgcccaggcggagctgcctcttctcccgcgg 155
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5852
287
1679
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US-08-488-011B-24
US-08-880-727-24
US-08-895-727-24
PCT-US95-10202-24
PCT-US95-10202-24
PCT-US95-10202-24
PCT-US95-1020-27
US-08-365-486A-11
US-08-382-766A-21
US-09-488-671-10
US-09-488-671-10
US-09-108-584A-8
US-09-078-294-4
US-09-078-294-8
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                                                                                                                                                                                                                                                                      0;
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Sequence 2, Appli
Sequence 27, Appli
Sequence 11, Appli
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Sequence 10, Appli
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Sequence 4, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 11, Appl
Sequence 26, Appl
Sequence 10, Appl
Sequence 10, Appl
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Sequence 18, Application US/08152443A Patent No. 5663070
                                          RESULT 3
US-08-152-443A-18
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; LOCATION:
US-08-444-231-18
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
                                                                                                                  2154 ctcccgcgg 2162
                                                                                                                                           2094 ggcactggcacggaacacacccttgaggccagccctggctgcccaggcggagctgcctctt 2153
                                                                                                                                                                                                   2034 gacgettetggggagtgagggaageggtttaegagtgaettggetggageeteaggggeg 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/152,443
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
TELEPAX: 7764,41
                                                                                                 121 CTCCCGCGG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 2471 base pairs Type: nucleic acid
                                                                                                                             61 GCACTGGCACGGAACACACCCTGAGGCCAGGCCCTGGCTGCCCAGGCGGAGCTGCCTCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                     1 GACCCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,231
FILING DATE: 18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              129;
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CITY: Palo Alto
STATE: Callfornia
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Sequence 1, Application US/08219237B
Patent No. 5874546
FORMERL INFORMATION:
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Best Local Similarity 100.0%; Score 129; DB 1; I Matches 129; Conservative 0; Mismatches 0;
APPLICANT: NAGATA, Shigekazu
APPLICANT: TOH, Naoto
APPLICANT: TOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                              2154 ctcccgcgg 2162
                                                                                                                                                                                                                                                                                                   2034 gacgottctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
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FEATURE:
NAME/KEY:
LOCATION:
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APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                           61 GCACTGGCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTT 120
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                                                                                                                                                                                                                                                                                      FEATURE:
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LENGTH: 2471 base pairs
TYPE: nucleic acid
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TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: LEHNHARDT, SUSAN K. REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 236
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## us-09-834-291-4.rni

Qy 2034 94090000 3300	4.6%; Score 129; DB 2: ry Match No. 2.3e-26 t Local Similarity 100.0%; Pred. No. 2.3e-26 tches 129; Conservative 0; Mismatches 0; ches 129; Conservative 0; Mismatches 129; Conservative 0; Mismatches	yA_site 82523 NETHOD: by similarity with NETHOD: to an established NETHOD:	FEATURE: polyA_site FEATUR	(EY: polyA_site (IN: 18311836) by similarity with (IFICATION METHOD: to an established (IFICATION METHOD: to an established (IN: IN: IN: IN: IN: IN: IN: IN: IN: IN:	FEATURE: mat_peptide NAME/KEY: mat_peptide LOCATION: 2431199 LOCATION METHOD: by similarity with known se IDENTIFICATION METHOD: to an established consensus IDENTIFICATION METHOD:	EY: sig_peptide ON: 195242 FICATION METHOD: by similarity with known FICATION METHOD: to an established consens	PEATURE: CDS. NAME/KEY: CDS. 10CARTION: 195.1202 DENTIFICATION METHOD: by similarity with known se IDENTIFICATION METHOD: to an established consensus IDENTIFICATION METHOD:	ORIGINAL SOURCE: ORGANISM: Homo sapiens IMMEDIATE SOURCE: LIBRARY: PCEV4 LIBRARY: pCEV4 CLONE: clone pF58	STRANDEDNESS: double STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA	OR SEQ ID NO: ARACTERISTICS: 2534 base pair: cleic acid	CLASSIFICATION PROPRATION: ATTORNEY_AGENT INFORMATION: ATTORNEY_James W. Hellwege NAME: James W. Hellwege REGISTRATION NUMBER: 28,808 REGISTRATION NUMBER: 516762 REFERENCE/DOCKET NUMBER: 516762	CLASSIFICATION DATA: PRIOR APPLICATION NUMBER: US 07/872,129 APPLICATION NUMBER: 1992 FILING DATE: 22-APR-1992 FILING DATE: 435	SOFTWARE: FACE  SOFTWARE: FACE  CURRENT APPLICATION NUMBER: US/08/219,237B  APPLICATION NUMBER: US/08/219,237B  APPLICATION NUMBER: US/08/219,237B  FILING DATE: 28 MAR-1994  FILING DATE: 435	ZIP: 2200 COMPUTER READABLE FORM: COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: Release #1.0, Version #1.25	# E
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Patent No. 6270998
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US-08-468-560C-1
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COMPUTER READABLE FLORPY disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: BLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PATCH Release #1.0, Version #1.30
OPERATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION MADER: US/08/468,560C
APPLICATION MUMBER: US/08/468,560C
APPLICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: GERIAD M.
NAME: MIDDER TE CEPTAD M.
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TITLE OF INVENTION: ANTIGEN

TORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.

CITY: FALLS CHURCH

CITY: FALLS CHURCH
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APPLICANT: TTOH, NAOCO
APPLICANT: YONEHARA, Shin
APPLICANT: YONEHARA, SAN
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TELEPAX: 703-205-8050
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REGISTRATION NUMBER: 20.7
REFERENCE/DOCKET NUMBER: 20.7
REFERENCE/DOCKET NUMBER: 20.7
TELEPHNNE: 703-205-8000
TELEPHNNE: 703-205-8000
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ORGANISM: Home
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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LOCATION:
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                                            FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                               LOCATION:
LOCATION:
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195..242
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E: cDNA to mRNA
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243..1199
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195..1202
                                                                                                                                                                                                                                                                                                          polyA_site
1831..1836
                                                                                                                                                          polyA_site
2352..2357
                polyA_site
2518..2532
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US-08-468-560C-1
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Matches 129; Query Match

Watch 4.6%; Score 129; DB 4; Length 2534; Local Similarity 100.0%; Pred. No. 2.3e-26; Length 2534; hes 129; Conservative 0; Mismatches 0; Indels

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APPLICANT: NAKAMURA, No. 630639510

APPLICANT: NAKAMURA, No. 630639510

ITILE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE FILE REFERENCE: 1110-207P

CURRENT APPLICATION NUMBER: US/09/180,100

EARLIER APPLICATION NUMBER: PCT/JP97/01502

EARLIER FILING DATE: 1999-11-02

EARLIER FILING DATE: 1997-05-01

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0

LENGTH: 2534

TYPE: DNA

ORGANISM: Homo sapiens
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
NUMBER OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE ADDRESS:
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                 US-08-232-463-14
                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                      Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 129; Conservative
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                                                                                                                                                                                                                                                                                2154 ctcccgcgg 2162
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                                                                                                                                                                                                                                                   121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09180100
Patent No. 6306395
                                                                                                                                                                                                                                                                            61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                      1 gacgettetggggagtgagggaageggtttaegagtgaettggetggageeteaggggeg 60
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1466 GCATAGATA 1474
                  Matches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/93
PILING DATE: 26-AUG-1991
APPLICATION NUMBER: EP 91 11.
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 39.768
TELECOMMUNICATION INFORMATION:
TELEFAN: (703)836-9300
TELEX 899149
INFORMATION FOR SEQ ID NO: 14:
LENGTH: 7218 DASE DASE
TYPE: NUCLEIC SCIP DAIRS

TYPE: NUCLEIC SCIP DAIRS
                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                        694 acattittitattiaaatgaacttittcattitggaatagtittiaggaittcaaaaaatti 753
                                                                                  514 aatgataagtattaagtaaggaagatccacatatgtgagttgctggcttataattcacac 573
                                                                                                                                                                                                                   454 tttggotacatttttttatttgtaaagtaagtttaataatcactcatctcactgggctat 513
                                                                                                                                                                                                                                                       394 tttaattootgactotgctatttattaactaaccatctttgccaatgttgcttaagcttt 453
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                       Match 2.8%; Score 79.4; DB 1; Length 7218; Local Similarity 5.4%; Pred. No. 4.9e-12; Length 7218; Les 20; Conservative 224; Mismatches 125; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPPRAD DE. DOS-TOS-TOS
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ZIP: 22313-0299
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US-08-232-463-14/c ; Sequence 14, Application US/08232463 ; Patent No. 5670367

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US-08-232-463-14
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CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO: 14:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                 807 ttgtgtctattagatgctcagagtgtgtgcacaaggctggcacgcccagggtcttcctca 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                            867 tggcactaacagtctactgaaaggtggaacagagacaagcctatcaacacctacaagact 926
1107 taattgggaagggagagggttgcagagtgcagagcttggtggacgatgccaaag 1166
                                                      1047 ctgaaggatgaacagtgggctaagcaaagggttattaatgtgttattaatgggttgaatc 1106
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                                                                                                                                    987 cotaacotagatttgagggcccaaacaggctccagaagaaaaatgtcaactgagaggaagc 1046
                                                                                                                                                                                         927 ggtggtmagtgcagtgacagatgcmamaacacagggtgatggamagccctcaggagggtma 986
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                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                  2.4%; Score 67.4; DB 1; Length 7218; Similarity 8.0%; Pred. No. 1.2e-08; 35; Conservative 228; Mismatches 174; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Gaps

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US-08-836-022A-10
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                                                                                                                                                                                                                                                                                    US-08-836-022A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                               Db 16048 CCGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACGCGGACATGTACAGA 16107
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                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
APPLICANT: Chen, Shu-Jen
APPLICANT: Weitzman, Matthew
APPLICANT: Weitzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
                                                                                                                                                                                              Best Local Similarity Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPTWARE: PATENTIA RE-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,022A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: US 08/331,381
FILING DATE: 28-OCT-1994
16168 TTTACAACGTCGTGACTGGGAA 16189
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 215-540-9200
                                                               16108 GCTCGAGAAGTAGTGGGCCACGTGGGCCGTGCACCTTAAGCTTGGCACTGGCCGTCGT 16167
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: cDNA
                                                                                 2174 gctcgagaagtactagtggccacgtgggccgtgcaccttaagctttagggtcgctggagg 2233
                                                                                                                                                    2114 cotgaggocagcoctggotgcocaggoggagctgcotottotocogoggacatgtacaga 2173
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CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                             2234 gggaccccggttggagagagga 2255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME:
                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19477
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                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spring House Corporate Cntr, P O Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trustees of the University of Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                              double
                                                                                                                                                                                                                        2.2%; Score 63.6; DB 3; Length 19307; 65.5%; Pred. No. 2.7e-07;
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                                                                                                                                                                                                               0
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                                                                                                                                                                                                                      Indels
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RESULT 11
US-08-836-022A-3/c
; Sequence 3, Application US/08836022A
; Patent No. 6001557
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: GNVPN.008PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-9200

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                             16168 TTTACAACGTCGTGACTGGGAA 16189
                                                                                                                                                                         16108 GCTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTGGCACTGGCCGTCGT 16167
                                                                                                                                                                                                                                                      16048 CCGCCCGCCTGCAGCTGGCCCCATCGATACCCGTACCTCGCGGACCCGCGGACATGTACAGA 16107
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                                                                                                                                                 2234 gggaccccggttggagagagga 2255
                                                                                                                                                                                                2174 gctcgagaagtactagtggccacgtgggccgtgcaccttaagctttagggtcgctggagg 2233
                                                                                                                                                                                                                                                                             2114 cctgaggccagccctggctgcccaggcggagctgcctcttctcccgcggacatgtacaga 2173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09427048A Patent No. 6203975
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/427,048A
FILING DATE: 21-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION CUNknown>
PRIOR APPLICATION ONTA:
                                                                                                                                                                                                                                                                                                                                       Match 2.2%; Score 63.6; DB 4; Length 19307; Local Similarity 65.5%; Pred. No. 2.7e-07; es 93; Conservative 0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weitzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Trustees of the University of Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/836,022 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Spring House Corporate Cntr, P O Box 457 STATE: Pennsylvania
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Fisher, Krishna J.
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US-09-427-048A-3/c
; Sequence 3, Application US/09427048A
; Patent NO. 6203975
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9972 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
APPLICATION NUMBER: US/08/836,022A
                                                                                                                                                                                                                                                             2860 TTACAACGTCGTGACTGGGAA 2840
                                                                                                                                                                                                                                                                                              2235 ggaccccggttggagagagga 2255
                                                                                                                                                                                                                                                                                                                     2920 CTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTGGCACTGGCCGTCGTT 2861
                                                                                                                                                                                                                                                                                                                                      2175 ctcgagaagtactagtggccacgtgggccgtgcaccttaagctttagggtcgctggaggg 2234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,381
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAK, MATY E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
TITLE OF INVENTION: Improved Adenovirus Virus and Methods of Use Thereof
                                                     APPLICANT: Trustees of the University of Pennsylvania Wilson, James M.
Fisher, Krishna J.
Chen, Shu-Jen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Trustees of the University of Pennsylvania APPLICANT: Wilson, James M. APPLICANT: Fisher, Krishna J. APPLICANT: Chen, Shu-Jen APPLICANT: Weitzman, Matthew TITLE OF INVENTION: Improved Adenovirus Virus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
)EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9972 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Howson and Howson
Spring House Corporate Cntr, P O Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.2%; Score 62.6; DB 3; Length 9972; 65.2%; Pred. No. 3.4e-07; 111ve 0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNVPN.008PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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0;

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson

COUNTRY: USA

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COMPUTER RADABLE FORM:

MEDIUM TAPE: FLOPPY disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC DOS/MS-DOS
OPERAPING SYSTEM: PC-DOS/MS-DOS
OPERAPING SYSTEM: PC-DOS/MS-DOS
OPERAPING SYSTEM: PC-DOS/MS-DOS
COPERATION DATA:
CURRENT APPLICATION NUMBER: US/09/427,048A
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: OR/636.022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/836,022

FILING DATE: <UNKNOWN>
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION UNMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVPN.008PCT
REFERENCE/DOCKET NUMBER: GNVPN.008PCT
TELEPHONE: 215-440-9200
TELEPHONE: 215-440-9200
TELEPHONE: 215-460-9200
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                                                                                                                                       TITLE OF INVENTION: MICROSIAL PRODUCTION OF 1,2-PROPANEDIOL TITLE OF INVENTION: FROM SUGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Spring House Corporate Cntr, P O Box 457 CITY: Spring House STATE: Pennsulvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score 62.6; DB 4; Length 9972;
pred. No. 3.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
ORGANISM: Vectors of the vectors of the vector of the vectors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-498-599-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; sequence 2, Application US/09498599 ; patent No. 6303352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2115 ctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgggacatgtacagag 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/801,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            523 CGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCCGCGGACATGTACAGAG 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cameron, Douglas APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
APPLICANT: ATTOROPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross & Stevens S.C.
ATREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: FROM PC COMPATIBLE

COMPUTER: COMPATION PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

SOFTWARE: PatentIN DATA: (A) 100 FC0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MI
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Madison
                                                                                                                    CLASSIFICATION:
                                                                                                                                                FILING DATE:
                                                                                                                                                                          APPLICATION NUMBER: US/09/498,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4476 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           circular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL FROM SUGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09820.037
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                                                           09820.037
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0;

US-09-427-048A-3

Query Match Matches

Local

h 2.2%;
Similarity 65.2%;
92; Conservative

TELERAX: 215-540-8818
TELERAX: 215-540-8818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 9972 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic double

TOPOLOGY: unknown MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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RESULT US-08-801-344-2

13

sequence 2, Application US/08801344 patent No. 6087140

GENERAL INFORMATION:

APPLICANT: Cameron, Douglas C. APPLICANT: Shaw, Anita J. APPLICANT: Altaras, Nedim E. APPLICANT: Altaras, Nedim E.

CORRESPONDENCE ADDRESS NUMBER OF SEQUENCES:

STREET:

Madison WI U.S.A.

STATE:

COUNTRY: U.S.A. ZIP: 53717-1914

ADDRESSEE:

E: DeWitt Ross & Stevens S.C. 8000 Excelsior Drive, Suite 401

TELEPHONE:

608-831-2100

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US-08-306-691B-19
                                                 INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGIH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-306-691B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/08306691B Patent NO. 5734039
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Vectors of the vector of the ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15 106,691B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS: 55
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, p.C.
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 78;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: birolage
MOLECULE TYPE: NOA (genomic)
ANTI-SENSE: NO
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APPLICANT: Skorski, Tomasz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2175 ctcgagaagtactagtggccacgtgggccgtgcaccttaagctt 2218
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                                    linear
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V: 514
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                                                                                                                                                               Ouery Match 2.1%; Score 59.8; DB 1; Length 35100; Best Local Similarity 55.6%; Pred. No. 4.7e-06; Matches 115; Conservative 0; Mismatches 92; Indels 0;
3986 TICTTTCTTTTTCTATCTTTTTGAGA 4012
                              3806 GAGGTTGCAGTGAGATGATGCCACTGCACTCCAGCCTAGGCGACAGAGCAAGACT 3865
              714 acttttcattttggaatagttttagga 740
                                            594 caattgtcctttaccctttttttctctctctccctccttccattccattccttctctctccctc 653
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Search completed: September 7, 2002, 18:29:19 Job time: 29253 sec

metastasis a

immune syste immune syste

genom

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OM nucleic - nucleic search, using sw model
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                         Result
                                                                                                                                             No.
                                                                                                                                                                                                               pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
1372.8
879.4
856.8
190.4
116.1
129
129
129
                                                                                                                                               Score
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1 tgaggactctcaggaatatg......tggctaatcaaagagacgtg 2827
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Copyright (c) 1993 - 2000 Compugen Ltd.
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| SIDSI/gcgdata/h|
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| SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:*
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| SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
| SIDS1/
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Listing first 45 summaries
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    48.6
31.1
30.3
6.7
5.7
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4.6
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266
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2471
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ABL34419
ABL34418
AAC98177
                                       AAC61798
AAC93879
              AAQ29959
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Human CD95 recepto
Human CD95 recepto
DNA encoding a hum
Fas-delta-TM CDNA.
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Human cell surface
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54.4
54.6
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556
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24259
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/note= "Fas gene promoter region"
147..151
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                       /function= GF1 transcription factor binding site /note= "Claim 7"
                                                                       /function= Myb transcription factor binding site
/note= "claim 9"
349..353
                                                                                                                                /function= EBP20 transcription factor binding site 272...276
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Human c-fms oncoge
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Human polynucleoti
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Murine LOBO homolo
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EP-892047 Seq ID 4
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Query Match
Best Local Similarity
                                                                                             Matches 1388;
                                                                                                                                                                                                                                                                                                                                                                          A novel DNA segment (AAT34162) has an isolated sequence region defined as the Fas gene promoter region. This includes a number is also included. The DNA segment was isolated from a human peptide corresponding to nt 23-346. It can be combined with the gene is under the transcription factor binding sites. A coding sequence for placental DNA library using a 32P-labeled segment of human Fas contact the gene is under the transcription factor binding sites. The promoter region can be transcription factor binding sites. The promoter region can be used a means of treating Fas mediated apoptosis disorders such as malionancies and antoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             827 gagtgtgtgcacaaggctggcacgcccagggtcttcctcatggcactaacagtctactga 886
                                  767 agagaatgcccatataccatcottatcccacttctttttgtgtctattagatgctca 826
                                                                                                                            Sequence 1608 BP; 398 A; 421 C; 423 G; 366 T; 0 other;
                       7 acagagatgecetataceatectecttateceacttetttttgtgtetattagatgetea 66
                                                                                                                                                                                                                                                                                                   Claim 11; Fig 2; 123pp; English.
                                                                                                                                                                                                                                                                                                                      Human Fas gene promoter region - used for heterologous protein expression and for developing products for treating Fas-mediated
                                                                                                                                                                                                                                                                                                                                                                                                 Cheng J, Koopman WJ, Liu C, Mountz JD,
                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR99471
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                                                                                             48.68;
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1497..1608
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/note= "claim 5"
1037...1043
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521..525
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                                                                                    Score 1372.8; DB 17; Length 1608; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO: 2392.
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                 WPI; 2002-130909/17
                                                                                                                                                                                                                                                             Olek A,
                          The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and including eye diseases such as retinopathy, neovascular acute myeloid including eye diseases, atterioscierosis, anaemia, cancer, acute myeloid including eyeneration, arterioscierosis, anaemia, neurofibromatosis, macular degeneration, arterioscierosis, anaemia, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                             cytosine methylation
                                                                                                                                                  Claim 1; SEQ ID NO 2392; 32pp + Sequence Listing; German.
 Sequence 1608 BP; 366 A; 51 C; 421 G; 770 T; 0 other;
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The present invention provides a number of human immune system associated can be used in the diagnosis and treatment of immune system disorders,
                                                                                 Claim 1; SEQ ID NO 2391; 32pp + Sequence Listing; German.
                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
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799 acgittgigagitttttatgitgtagttataagatggatagtttagttaaaigtttcgta 858
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                                                                                                                                                                                                                                                                                          499 titatyttaaattatttaagayttatttatcytittaaagtaatagtgattitgaatagt 558
                                                                                                                                                                                                                                                                                                                                                        1199 aactgcatccaaattcaggttcagtaatgatgtcattatccaaacataccttctgtaaaa 1258
                                                                                                                                                                                                                                                                                                                                          439 aattytatttaaatittaggittagtaatgatgittattatttaaatatattitittgiaaaa 498
                                                                                                                                                                                                                                                                                                                                                                                                     1139 gtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtgtgtccagtctgg 1198
                                                                                                                                                                                                                                                                                                                                                                                        379 ytgtagagtttggtggacgatgttaaaggaatartgaaatttttagtgtgtttagtttgg 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1079 tattaatgtgttattaatgggttgaatctaattgggaagggagagggtggcagagtgag 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                     319 tattaatgigttattaatgggttgaatttaattgggaagggagagagggitgtagagtgag 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1019 cagaagaaaatgtcaactgagaggaagcctgaaggatgaacagtgggctaagcaaagggt 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 tagaagaaatgitaatigagaggaagittgaaggatgaatagiggitaagtaaagggt 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   959 gggtgatggaaagccctcaggagggtaacctaacctagatttgagggcccaaacaggctc 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 agataagtttattaatatttataagattggtggtaagtgtagtgatagatgtaaaatata 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 899 agacaagcctatcaacacctacaagactggtggtaagtgcagtgacagatgcaaaacaca 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                839 aaggetggeaegeeeagggtetteeteatggeaetaacagtetaetgaaaggtggaacag 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              779 tataccatcctccttatcccacttcttttgtgtctattagatgctcagagtgtgtgcac 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1608 BP; 398 A; 51 C; 423 G; 736 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 aagyttggtacgtttagggtttttttttatggtattaatagtttattgaaaggtggaatag 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.3%; Score 856.8; DB 24; 76.7%; Pred. No. 4.6e-226; ative 0; Mismatches 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _DB_24; Length 1608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acute myeloid
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                                RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                          AAC98177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1679 gogototgagotocattotocttcaagacotococaacttcccaggttgaactacagcag 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1799 gccactgcaggaacgccccgggacaggaatgcccatttgtgccaccgaaccctgactcctt 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1038 gttattgtaggaacgtttcgggataggaatgtttatttgtgtaacgaattttgatttttt 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1859 cctcaccctgacttctccccctccctacccgcgcgcaggccaagttgctgaatcaatgga 1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1979 gettttegtgagetegtetetgatetegegeaagagtgacacacagggtgtteaaagaege 2038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1098 ttttattttgattittttttttttttattcgcgcgtaggttaagttgttgaattaatgga 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2099 tggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctctcccc 2158
                                                                                                                                                                                                                                                                                                                                                                                                                                       1398 gcgg 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2159 gcgg 2162
                                                                                                                                                                                                                                                                                                                                                                                 AAC98177 standard; cDNA; 859 BP.
                                                                                                                                                                                                                                                                                                                                     09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                           AAC98177;
                                                                                                                                                                                                                                                                                        Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                             Human colon cancer antigen nucleotide sequence SEQ ID NO:187.
                                                                                                                                                                                                                                                    identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                  neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aagootttagaaagggcaggaggccggctctcgaggtcctcacctgaagtgagcatgcca 1798
                                                                                                                                                                         WO200055351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aagtttttagaaagggtaggaggtoggtttttogaggttttttatttgaagtgag-atgtta 1037
                                                                                                                          08-MAR-2000; 2000WO-US05883.
                                                                                                                                                  21-SEP-2000.
                                                                                                      12-MAR-1999;
colon cancer associated gene sequences, referred to as colon cancer
                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Ruben SM;
                      P-PSDB; AAB53420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtttttcgtgagttcgtttttgatttcgcgtaagagtgatatataggtgtttaaagacgt 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttotggggagtgagggaagcggfttacgagtgacttggctggagcctcaggggcgggcac 2098
                                    2000-587534/55.
                                                                                                          9905-0124270
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AAAC97991 to AAC98763 encode the human colon cancer associated proteins, AAAC97991 to AAC98763 encode the human colon cancer antigens, given in AAB53234 to AAB54006. The CC called human colon cancer antigens can have cytostatic, cardioactive, muscular; CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal, cc can be used in gene therapy. The colon cancer antigen polynucleotides, and be used in disposition of the proteins are useful for the prevention, cc can be used in disposition of the proteins are useful for the prevention, cc proteins and antibodies to the proteins are useful for the prevention, such as for cc proteins and disposition of colon dispositions are useful for the prevention, cc polynucleotides may be used in disposition and research, such as for cc polynucleotides may be used in disposition and research, such as for cc gystem disorders, muscular disorders, such as neural disorders, immune cc gystem disorders, muscular disorders, reproductive disorders, infectious gystem disorders, wounds, renal disorders, infectious gastrointestinal disorders, wounds, renal disorders, infectious and cardiovascular disorders. AAC98772 and cardiovascular disorders. AAC98772 and cardiovascular disorders. AAC98772 and cardiovascular disorders.
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Matches 197; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 610-611; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 859 BP; 214 A; 219 C; 227 G; 193 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1955 cttcccatcctcqaccaccqqqqcttttcqtqagctcgtctctqatctcqcqcqcaaqaq 2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2015 tgacacacaggtgttcaaagacgcttctggggagtgaggggaagcggtttacgagtgactt 2074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2135 ccaggcggagctgcctcttctcccgcgg 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 ggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccctggctgc 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 cytecyccaegogtecyaecygygettttegtgagetegtetetgatetegegeaagag 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                     AAZ88700 standard; DNA; 266 BP
                                                                                                                                                                                                                                                                                                                     11-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                         AAZ88700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 ccaggcggagctgcctcttctcccgcgg 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 tgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacgagtgactt 138
                                                                                                                                                                                                                                          cancer chemotherapy; ss.
                                                                                                                                                                                                                                                        p53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                                                                                                      Human CD95 receptor intron 1 fragment.
                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                          protein_bind
                                                                                                                                                                            Key
                                                                 03-FEB-2000
                                                                                             DE19847779-C1.
 16-OCT-1998;
                                 16-OCT-1998;
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       98DE-1047779.
                                      98DE-1047779.
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                  /bound_moiety= p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 190.4; DB 21; Length 859; Pred. No. 5.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-628395/60
                                Dean NM,
                                                    (ISIS-) ISIS PHARM INC.
                                                                                                          10-APR-2000; 2000WO-US09540
                                                                                    12-APR-1999;
                                                                                                                                             19-OCT-2000.
                                                                                                                                                                        WO200061150-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                       Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis; Fas associated protein 1; protein tyrosine phosphatase; cancer; autoimmune disease; inflammatory disease; lymphoma; ss.
                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       DNA encoding a human Fas (Apo-1) protein.
                                                                                                                                                                                                                                                                                                                                                                         06-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           AAC61798 standard; DNA; 2551 BP;
                                                                                                                                                                                                                                                                                                                                                                                                               AAC61798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2333 gcgggggcggggagagagcctgcagccttcagaacagatat 2373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2213 aagetttagggttggtggagggggaccccggttggagaggaggggaactcctggacaa 2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 gcggggggggggagagagcctgcagccttcagaacagatat 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor intron 1 which contains a p53 binding region described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 aagctttagggtegetggaggggaeeeeggttggagaggaggageggaaeteetggaeaa 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 4; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-162245/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krammer P, Mueller-Schilling M, Oren M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                          Marcusson EG;
                                                                             9908-0290640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                             /product= "Fas"
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 161; DB 21;
100.0%; Pred. No. 3.3e-34;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 266;
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                                                      (LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                        15-NOV-1993;
                                                                                                                                                                        15-NOV-1994;
                                                                                                                                                                                                                            26-MAY-1995.
                                                                                                                                                                                                                                                                               W09513701-A.
                                                                                                                                                                                                                                                                                                                                                               mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fas-delta-TM; transmembrane deletion; apoptosis; antibody; adoptive immunotherapy; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fas-delta-TM cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ93879 standard; cDNA; 2471 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2128 tggctgcccaggcggagctgcctcttctcccgcgg 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2068 gtgacttggctggagcctcaggggggggggcactggcacgggacacacccctgaggccagccc 2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2008 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 2067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 tygctgcccaggcggagctgcctcttctcccgcgg 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region, translational start site, translational termination region or 3'-untranslated region of nucleic acid molecules encoding Fas, Fa sociated protein 1, protein tyrosine to treat autoimune or inflammatory diseases such as hepatitis. They are used to the used to treat cancer, especially colon, liver or lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes human Fas (Apo-1). The specification describes antisense compounds which are targeted to the 5'-untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 71-73; 116pp; English.
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                                                                                                            93US-0152443.
                                                                                                                                                                94WO-US13173
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                                                                                                                                                                                                                                                                                                                                           /*tag= b
243..1136
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195..242
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Shapiro JP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 2551;
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AAX24878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding Fas protein without its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Fas mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA was obtd. from human lymphocytes and PCR was used to make cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCR product was ligated into pBluescript and the recombinant plasmid was used to transfect E. coli DH5-alpha cells. insert sequence of pBluescript-Fas-delta-TM is glyen in AAQ93879.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2034 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soluble Fas receptor DNA.
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                                                                                                                                                                                                                                                             polyA_signal
   17-JUL-1997;
                                                          16-JUL-1998;
                                                                                                                 28-JAN-1999.
                                                                                                                                                                           WO9903999-A1
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243..1136
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2455..2460
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100.0%; Pred. No. 9e-25;
ative 0; Mismatches 0;
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of Fas ligand (Fash). In some embourance of the cell mixture comprises with the immunosuppressive agent, and the cell mixture comprises of neutrophil cells. The method can be practised in vitro, ex vivo or in vivo. Suitable immunosuppressive agents include antisense in vivo. Suitable immunosuppressive agents include antisense in concern that inhibit endogenous FasL expression, soluble Fas. Conceptors, ribozymes that inhibit the endogenous expression of receptors, ribozymes that inhibit the endogenous expression of condended the endogenous expression of transforming growth factor (TGF)-beta, condogenous expression of transforming growth factor (TGF)-beta, conding for an immunosuppressive agent such as and polynucleotides coding for an immunosuppressive agent such as conditional conditions and polynucleotides coding for an immunosuppressive agent such as conditional conditions and polynucleotides coding for an autolimnune disease such as graft versus host disease, or an autolimnune disease such as considered invention also provides a method for identifying agents which the invention also provides a method for identifying agents which condulate FasL stimulation of a proinflammatory response.
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AAQ29959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This present sequence is a DNA clone encoding soluble Fas receptor (see AAW98070). The invention provides a method for inhibiting an proinflammatory response in a cell mixture by administering an immunosuppressive agent which inhibits the proinflammatory activity of Fas ligand (Fasi). In some embodiments, Fasi is coadministered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-132243/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2034 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
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                                                                                                                                                                                                                                                                                                       AAQ29959 standard; cDNA to mRNA; 2534 BP.
                                                                                                                                                                                                                               12-MAR-1993 (first entry)
                                                                                                                                               Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss
                                                                                                                                                                                          Human cell surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                        121
                  mat_peptide
                                                     sig_peptide
                                                                                                                Homo sapiens.
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                    /*tag= a
243..1199
                                                         Location/Qualifiers
195..242
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100.0%; Pred. No. 9e-25;
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Best Local
                     19-FEB-1996 (first entry)
                                                    AAQ95297;
                                                                      AAQ95297 standard; cDNA; 2534 BP.
                                                                                                                                                                                                                                                                                                                                                                                 A cDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The CDNA was ligated to BstXI-cut vector pCEV4 via BstXI linkers. The KT3 cDNA library was used to transfect monkey COS-Ab. The cells which were then suspended in buffer containing murine anti-Fas antibodies. The Fas-expressing cells aftered with goat anti-mouse Extrachromosomal DNA was prepared from adhered to the plates. transform E.coli VM100 cells. A 520bp XhoI-BamHI fragment from a positive clone (pF3) was used to screen the KT-3 cDNA library. The to a 335 amino acid pre-protein and a 319 amino acid mature protein of the human Fas antigen.
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                                                                                                                                                                                                                                             2034 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
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                                                                                                                                       121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monocional antibodies that react with tumour cells expressing Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Fig 1 and 2; 27pp; English.
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                                                                                                                                                                                                                               1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcagggggcg
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2352..2357
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2518..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= Fas_antigen
1046
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                                                                                                                                                                                                                                                                                                          100.0%;
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Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; rheumatoid arthritis; serum; systemic lupus erythematosus; ss.
                                          hFas coding sequence from plasmid pCEV4/hFas.
                                                                                                                         AAT16303 standard; cDNA; 2534 BP.
                                                                            06-SEP-1996
                                                                                                        AAT16303;
                                                                                                                                                                                                           2154 ctcccgcgg 2162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ95297 is the plasmid pF58 which contains the human Fas cDNA. The plasmid was used in the construction of an expression vector for the prodn. of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of
                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Pages 15-17; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparation of soluble membrane proteins - for their use in antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR78606.
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                                                                                                                                                                                                                                       61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
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                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pF58; human Fas cDNA; soluble membrane protein; antibody production; diseases; treatment; prevention; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pF58 contg. human Fas cDNA.
                                                                                                                                                                                                                                                                                            1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                       99cact9gcac9gaacacaccctga9gccagccctggctgcccaggcggagctgcctctt 2153
                                                                                                                                                                                              ctcccgcgg 129
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-0267644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93JP-0267644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
243..1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195..242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195..1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                   4.68;
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                               Score 129; DB 16;
Pred. No. 9.2e-25;
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Length 2534;
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                              60
            SLE;
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0,

CDS

/product= Fas antigen 195..242

Location/Qualifiers 195..1201

sig\_peptide mat\_peptide W09601277-A1

/\*tag= 243..1

.1998

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This sequence represents the coding sequence for the human Fas antigen is contained within the plasmid pCEV4/hFas. The soluble Fas antigen is contained within the plasmid pCEV4/hFas. The soluble Fas antigen contains an immobilised anti-soluble Fas antigen encoded included in the immunoassay kit of the invention. His antigen encoded included in the fas antigen and contains an immobilised antigen encoded assay of soluble Fas antigen and contains an immobilise Fas antigen encoded assay is simple and haber of different specimens by this sequence. The assay is simple and haber of different specimens sensitivity, and the capable of assaying a number of different specimens at the same time. The immunoassay is used on biological samples (such as sensitivity, and the immunoassay is used on biological samples section at the same time. The immunoassay is used on biological samples (such as serum) and is useful for diagnosis of autoimmine diseases such as rheumatoid arthritis or systemic lupus erythematosus (SLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoassay method for soluble Fas antigen in body fluids - for diagnosis of auto:immune diseases such as rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2534 BP; 817 A; 488 C; 502 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                     2034 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
                                                                                                                                                                                                                                                         2094 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2153
                                                                                                                                                                                                                                    61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                              1 gacgettetggggagtgagggaageggtttaegagtgaettggetggageeteaggggeg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6%; Score 129; DB 17;
100.0%; Pred. No. 9.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 2534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xx The present sequence represents a Ras cDNA sequence used in the content of the invention. The method is concerned with reducing (TK) the method of the invention. The method is concerned with reducing (TK) content of activated Fas-expressing CD8+ T-lymphocyte of Fas-ligand CC dells in an immune cell population which also comprises or activated CC (Fasi)-expressing activated CD4+ cells. It involves contacting this content of an agent (e.g. a cells in the fasi. Therefore, the method is useful for CC immune cell population which would interfere with the cell interfere the population protein) which would interfere with the cell interfere the population of activated CC interfered by the cells in immune cell populations. Also claimed interfered the populations of the agent in the manufacture of therapeutic compositions. CC identifying switable agent which can reduce depletion of the fas-expressing CD8+ TK cells in municature of the interaction of the graph covers and its ligand Fasi. By interfering with the use of tymphocytes can be triggered by Expression of Fasi on cell surface receptor Fas and its ligand Fasi. By interfering with cells interaction, the method described and its preparations can prevent cells interaction, the method described by expression of Fasi on cells interaction, the proposition with an immunodeficiency activated CD4+ cells. Such Fasi-expressing activated CD4+ cells are cells infection with an immunodeficiency virus (STV). The claimed prevention of tymphocytes (CTM) activity continues the CD4+ cells infection with the infectious agent, enabling the content of cytoxic T lymphocyte (CTM) activity content of cytoxic T lymphocyte (CTM) activity content of cytoxic the infectious agent, enabling the content of cytoxic the infectious agent, enabling content of cytoxic the infectious agent, enabling content of cytoxic the cytoxic the cytoxic the cytoxic than the cytoxic that the infectious agent, enabling the cytoxic than the cytoxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ras protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL; Fas protein; CD8+ T-lymphocyte; human immunodeficiency virus; GD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL; sinian immunodeficiency virus; SIV; cytotoxic T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophylactic; AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09835692-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency Reducing CD8+ lymphocyte apoptosis to treat e.g. with Fas-ligand diseases - by interfering with interaction of Fas with HIV expressed on activated CD4+ cells, e.g. cells infected with HIV expressed on activated CD4+ cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screaton GR,
                     Š
                                                               Best Local similarity
Matches 129; Conserv
                                                                                                              Query Match
                                                                                                                                                                                Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-456867/39.
χu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97GB-0003276.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Fas protein"
195. 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195..1202
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1831..1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
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                                                                                         4.6%; Score 129; DB 19;
100.0%; Pred. No. 9.2e-25;
100.0%; Pred. No. 9.2e-25;
1tive 0; Mismatches 0;
                                                                                                                                                             DB 19; Length 2534;
                                                                                                                              Indels 0;
                                                                                                                                                Gaps
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δõ

Query Match Best Local S

Similarity

S 밁

g

2154 ctcccgcgg 2162

121 ctcccgcgg 129

AAV32993

AAV32993;

18-NOV-1998 Fas cDNA.

(first entry)

AAV32993 standard; cDNA; 2534 BP.

RESULT 12

03-MAR-1995; 18-JAN-1996.

06-JUL-1994; 14-FEB-1995;

(MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.

95JP-0025637. 94JP-0154706. 95WO-JP00349.

(NISB ) JAPAN TOBACCO INC

Noguchi J, Yonehara S;

WPI; 1996-087635/09.

systemic lupus erythematosus

Example 8; Page 49-52; 124pp; Japanese.

Дb

В

2094 99cactg9cac9gaacacacctgag9ccagccctggctgcccaggcggagctgcctctt 2153

1 9acgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60

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The present sequence was used in the development of novel Fas region lacking one or more amino acid residues in the region stracellular (preferably at least 29 residues are deleted). The derivatives are effective regulators of apoptosis and can be e.g. diabetes, arthritis, lupus and HIV, by modulating or by modulating the second of sease, arthritis, lupus and HIV, by modulating apoptosis of such as hepatitis, influenza and HIV, by modulating apoptosis of
Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;
                                                                                                                                              Disclosure; Fig 1-2; 102pp; Japanese.
                                                                                                                                                   Fas antigen derivative containing modified extracellular region of viral and other diseases
                                                                                                                                                                                                                    P-PSDB; AAW50289
                                                                                                                                                                                                                            WPI; 1997-558981/51.
                                                                                                                                                                                                                                                     Nagata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                            (MOCH ) MOCHIDA PHARM CO LTD.
(OSAB-) OSAKA BIOSCIENCE INST.
                                                                                                                                                                                                                                                                                                  02-MAY-1996;
                                                                                                                                                                                                                                                                                                                     01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                        13-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                          WO9742319-A1.
                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis modulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Fas antigen; derivative; apoptosis regulation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Fas antigen cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV07002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV07002 standard; cDNA to mRNA; 2534 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2154 ctcccgcgg 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 99cactggcacggaacacacctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                              Nakamura N;
                                                                                                                                                                                                                                                                                           96JP-0135760.
                                                                                                                                                                                                                                                                                                             97WO-JP01502.
                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
243..1199
                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
195..2
                                                                                                                                                                                                                                                                                                                                                                 /product= Fas_antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                . 242
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* 55555555555555
                                                                                                 Query Match
2114 cctgaggccagccctggctgcccaggcggagctgcctcttctcccgcggacatgtacaga 2173
                                                                                                                              Shuttle vector paddel.CMVDys (AAT27558) comprises the adenovirus is elements needed for replication and virion encapsidation but single under control of the CMV promoter. It is used with a helper infection but which has disabled packaging function. Recombinant delivery to host cells and the ability to stably integrate the fost cell chromosome. Such a vector can be used that is characterized by high titer transgene into the host cell chromosome. Such a vector can be used tharany function.
                                                                                                   Sequence 19307 BP; 4816 A; 4393 C; 4056 G; 6042 T; 0 other;
                                                                                                                                                                                                                                                                                      Example 9; Fig 12A-12P; 149pp; English.
                                                                                                                                                                                                                                                                                                 Recombinant adenovirus produced from shuttle vector and helper virus transgene(s) to target cells
                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-251463/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                   Chen S, Fisher KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                        (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09613597-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                       93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adenovirus type 5; Ad5; vector; gene therapy; gene transfer; helper virus; dystrophin; muscular dystrophy; ds; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.2%;
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shuttle vector pAdDel.CMVDys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT27558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT27558 standard; cDNA; 19307 BP.
                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2094 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2034 gacgettetggggagtgagggaageggtttacgagtgaettggetggageeteaggggeg 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 gaegettetggggagteagggaageggtttaegagtgaettggetggageetcaggggeg 60
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0331381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US14017.
                                                  2.2%; Score 63.6; DB 17; Length 19307;
                                                                                                                                                                                                                                                                                                                                                                                            Weitzman M,
                                                                                                                                                                                                                                                                                                                                                                                   Wilson JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 127.4; DB 1
Pred. No. 2.5e-24;
0; Mismatches 1
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AAT27557/c
ID AAT275
AC AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16108 gctcgagaagtactagtggccacgtgggccgtgcaccttaagcttggcactggccgtcgt 16167
                                                16168 tttacaacgtcgtgactgggaa 16189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2174 gctcgagaagtactagtggccacgtgggccgtgcaccttaagctttagggtcgctggagg 2233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2234 gggaccccggttggagagagga 2255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7557/C
AAT27557 standard; cDNA; 9972 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT27557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shuttle vector pAdDel.CBCFTRZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adenovirus type 5; Ad5; vector; gene therapy; gene transfer; helper virus; cystic fibrosis transmembrane conductance regulator; helper virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CETR; ds; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_unit
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                                                                                                                                                                                                                                                                                                     repeat_unit
                                                                                                                                                                                       09-MAY-1996.
                                                                                                                                                                                                                             W09613597-A2.
                                                                                                                                                  27-OCT-1995;
                                   Chen S, Fisher KJ, Weitzman M,
                                                                   (UYPE-) UNIV PENNSYLVANIA.
                                                                                                               28-OCT-1994;
WPI; 1996-251463/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_type= INVERTED inverted terminal repeat"
/note= 3, adenovirus inverted terminal repeat"
/note= 3887. 3684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3652..3073)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (9241..8684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "5' adenovirus înverted terminal repeat"
complement (9374..9360)
/*tao= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (9611..9254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function= CFTR gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function= CMV enhancer/beta actin promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function packaging sequence PAC I complement (9353..9340)
                                                                                                                                                                                                                                                                                                                                                                         /function= packaging sequence PAC III complement (9301..9288)
                                                                                                                                                                                                                                                                                                                                                                                                                               /function= packaging sequence PAC II
complement (9311..9298)
                                                                                                                                                               95WO-US14017.
                                                                                                                                                                                                                                                                                                             /function packaging sequence PAC IV complement (9276..9263)
                                                                                                                        94US-0331381.
                                                                                                                                                                                                                                                                             /function= packaging sequence PAC V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shuttle vector paddel.CBCFTR (AAT27557 comprises the adenovirus cis elements needed for replication and virion encapsidation but deleted of all viral genes. It carries a CFTR gene under the control of a chimeric CMV enhancer/chicken beta-actin production that supplies the sequences needed for it used with a helper virus that supplies disabled packaging function but which has disabled packaging that there is used wiral infection but which has disabled packaging that there a productive viral infection but which has disabled packaging titler the approductive viral infection and the solility to stably integrate the ranagene delivery to host cells and the such a vector can be used transgene into the host cell chromosome. Such a vector can be the to transfer the CFTR gene for use in cystic fibrosis gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant adenovirus produced from shuttle vector and helper virus - has crippled packaging function, useful for delivering transgene(s) to target cells
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
search completed: September 7, 2002, 18:43:03
yob time: 30077 sec
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9972 BP; 2581 A; 2362 C; 2245 G; 2784 T; 0 other;
                                                                                                                                                                                                                                                               2175 ctcgagaagtactagtggccacgtgggccgtgcaccttaagctttagggtcgctggaggg 2234
                                                                                                                                                                                    2920 CTCGAGAGAGTACTACTGGCCACGTGGGCCCGTGCACCTTAAGCTTGGCACTGGCCGTCGTT 2861
                                                                                                                                          2235 ggaccccggttggagagagga 2255
                                                                                                                                                                                                                                                                                                                                                   2.2%;

v Match 55.2%;

Local Similarity 65.2%;

Local Similarity 65.2%;

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Local Similarity 65.2%;
                                                                                                      2860 TTACAACGTCGTGACTGGGAA 2840
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 62.6; DB 17
Pred. No. 4.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17: Length 9972;
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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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| /cgn2_6/ptodata/2/pna/F
| /cgn2_6/ptodata/2/pna/U
| /cgn2_6/ptodata/2/pna/U
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us-09-834-291-4.rnpm
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31 US-08-377-522-1
7 US-08-34-291-2
8 US-09-36-350A-14682
17 US-09-91-62-14682
18 US-09-12-360-3367
56 US-09-652-124-8816
18 US-09-762-124-8816
25 US-09-762-124-8816
25 US-09-713-350-4919
26 US-09-726-172-2083
29 US-09-726-788-5939
29 US-09-726-788-5939
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29 US-09-726-810-2456
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56 US-60-213-360-1236
66 US-60-213-360-1236
67 US-09-287-618-11167
16 PCT-USU-09-25-299-187
34 US-09-25-299-187
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Sequence 3, Appli
Sequence 10, Appli
Sequence 1, Appli
Sequence 94, Appli
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Sequence 120, App
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Sequence 4 Application US/09834291
APPLICANT Krammer, Peter
APPLICANT Wuller Schilling, Martina
FILE OF INVENTION: D53 Binding Areas
CURRENT APPLICATION: D53 Binding Areas
CURRENT APPLICATION NUMBER: US/09/834,291
PRIOR APPLICATION NUMBER: D01-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: D01-018
NUMBER OF SEQ ID NOS: 32
SOFTWARRE. Date: 1998-10-16
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: HOMO Sapiens
US-09-834-291-4
                                                361 aagagcaggacettgggagcaagaatatetaagtttaatteetgaetetgetatttatta 420
                                                                           301 gaacttgaggataattagacgtacgtgggtagagggtagggggaagggggtatggcataga 360
                                                                                       301 gaacttgaggataattagacgtacgtgggtagaggggtagggggaagggggtatggcataga 360
                                                                                                                241 ctaagattatittgaccatgaaacatatgtotococcacaaagcacatattcctatotoctt 300
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                                                                                                                           241 ctaagattatttgaccatgaaacatatgtotocccacaaagcacatattcotatctcctt 300
                                                                                                                                                     181 taagggccctgagaagttttggattaagaaagttttcaaattaaagtaacccagaatttt 240
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US-09-817-500-2214
US-09-78-508-5938
US-09-52-124-5645
US-09-24-611-3879
US-09-94-809-3879
US-09-925-564-39624
US-09-726-788-4710
US-09-716-475-3862
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US-60-018-911-581
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RESULT 291-3  US-09-00-3, Application US/09834291  US-09-00-3, Application US/09834291  Sequent INFORMATION: P3 Binding Areas APPLICANT: APPLICANT: APPLICANT: APPLICANT: Sequent INFORMATION: P32 Binding Areas APPLICANT: APPLICANT: Sequent INFORMATION: P32 Binding Areas APPLICANT: Sequent INFORMATION: P33 Binding Areas APPLICANT: Sequent INFORMATION: P32 Binding Areas APPLICANT: Sequent INFORMATION: P33 Binding Areas Score 2380; DB 32: Length 2280; P810 Replicant: P32 Binding Areas APPLICANT: P33 Binding Areas APPLICANT: Sequent INFORMATION: P33 Binding Areas APPLICANT: P34 Binding Areas APPLICANT: P35 Binding Areas APPLICANT: P36 Binding Areas APPLICANT: P37 Binding Areas APPLICANT: P38 Binding Areas APPLICANT: P39 Binding Areas APPLICANT: P39 Binding Areas APPLICANT: P30 Binding Areas APPLICANT: P30 Binding Areas APPLICANT: P31 Binding Areas APPLICANT: P32 Binding Areas APPLICANT: P33 Binding Areas APPLICANT: P34 Binding Areas APPLICANT: P35 Binding Areas APPLICANT: P36 Binding Areas APPLICATION AREAS APPLICANT: P37 Binding Areas APPLICANT: P38 Binding Areas APPLICATION AREAS APPLICATION AREAS APPLICANT: P38 Binding Areas APPLICATION AREAS APPLICATION AREAS APPLICATION AREAS APPLICATION AREAS APPLICATION AREAS APPLICANT: P38 Binding Areas	2581 gactgtaagtcgctgctfl	

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Db 10934 gccttgtctcccttccgggaattctctctttaagactgtaagtcgctgcctgagtggttt 10993
    2608 cattttgttttgttttctgcccttctctttcttctttttgccctttcttagcttgcactc 2667
                                             10874 getgaatgagettetggaggettgtttacegttttttattgtcacacagaaaaggaaact 10933
                            2488 gctgaatgagcttctggaggcttgtttaccgttttttattgtcacacagaaaaggaaact 2547
                                                                                 2428 ggttaagccggagggctcggaagaacggcaccttttcttctcgaaaagttatatgggg 2487
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ORGANISM: HOMO Sapiens
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                                                                                                             301 gaacttgaggataattagacgtacgtgggtagagggtagggggaagggggtatggcataga 360
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Best Local Similarity 83.0.
Matches 2795; Conservative
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US-09-665-615B-94
                                                                 Query Match
Best Local Similarity 99.9%; Pred. No. 0;
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GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Wyatt, Jacqueline
FILE REFERENCE: ISPH-0502
CURRENT APPLICATION NUMBER: US/09/665,615B
PRIOR APPLICATION NUMBER: US/09/640
PRIOR ETLING DATE: 1999-0418
PRIOR ETLING DATE: 1999-040
NUMBER OF SEQ ID NOS: 1799-12
SOFTWARER: BATGETH US-79
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SEQ ID NO 94
447 aagettetttggetacattttttatttgtaaagtaagtttaataatcactcatctcact 506
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LOCATION: (1782)...(1813)
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                           ; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-802-669-94
                                                                                                                                             APPLICANT: Wyatt, Jacqueline
APPLICANT: Zhang, Hong
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TITLE OF INVENTION: UNMEER: US/09/802,669
CURRENT EPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US/09/665,615
PRIOR APPLICATION NUMBER: US/09/665,615
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 94
FILING DATE: 1999-04-12
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Query Match 60.6%;
Best Local Similarity 99.9%;
Matches 1715; Conservative
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                                                                                                  ORGANISM: Homo sapiens FEATURE:
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            0; Mismatches
                        Pred. No.
                                   Score 1714.4;
                                         В
                 1.
                                          31; Length 2165;
                   Indels
                       0; Gaps
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ATTORNEY/AGENT INFORMATION:
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                                  COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,522
CTICTOTALE: 20-TAN-1995
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MEDIUM TYPE: Floppy
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                                                                                                                                                                             STREET: P.O. Bo
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                    TITLE OF INVENTION: Human Fas Gene Promoter Region NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                 APPLICANT: Mountz, John D.
APPLICANT: Liu, Changdan
APPLICANT: Cheng, Jianhua
APPLICANT: Koopman, William J.
APPLICANT: Zhou, Tong
                   CLASSIFICATION:
                                                                                                            COMPUTER:
                                                                                                                                                      COUNTRY: US
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                1681 ctggctgcccaggcggagctgcctcttctcccgcgg 1716
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                     20-JAN-1995
N: 435
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1487 gggccctcccttttcagagccctatggcgcaacatctgtactttttcatatggttaactg 1546
                        US-08-377-522-1
                                                                             1367 ggccaggaaataatgagtaacgaaggacaggaagtaattgtgaatgtttaatatagctgg 1426
                                                                                                                        Query Match
48.6%; Score 1372.8; DB 7; Length 1608;
Best Local Similarity 99.4%; Pred. No. 2.4e-287;
Matches 1388; Conservative 0; Mismatches 7; Indels 1;
                                                                  607 GGCCAGGAAATAATGAGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAATATAGCTGG 666
                                                                                                            1187 tgtccagtctggaactgcaatccaaattcaggttcagtaatgatgtcattatccaaacata 1246
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                                                                                                                                                                                                                                                                                      427 TGTCCAGTCTGGAACTGCATCCAAATTCAGGTTCAGTAATGATGTCATTATCCAAACATA 486
                                                                                                                                                                                                                                              367 TTGCAGAGTGAGGTGCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTG 426
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SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
                                                                                                                                                                                                                                                                                                                                                                          127 AAGGTGGAACAGAGACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAG 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sertich, Gary J.
REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: U00-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512,418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                 CCAAACAGGCTCCAGAAGAAAATGTCAACTGAGGAAGGCAAGGCTGAAGGATGAACAGTGGGC 306
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DEDNESS: single
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US-08-377-522C-1
              1547 tccattccaggaacgtctgtgagcctctcatgttgcagccacaacatggacagcccagtc 1606
                                                                                                                                      Sequence 1, Application US/08377522C

GENERAL INFORMATION:
APPLICANT: Mountz et al.
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
Annumerocom
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                                                                                                                                                                                                                                1386 GCCTCTTCTCCCGCGG 1401
                                                                                                                                                                                                                                              2147 gcctcttctcccgcgg 2162
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
FILING DATE: January 20, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILTURE
                                                SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: 77071
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
                                                                                                                    CITY: Houston
                                                                                                                            STREET:
                                                                                                                                    ADDRESSEE:
                                       APPLICATION NUMBER: US/08/377,522C
FILING DATE:
                                                                                                                             E: Benjamin Aaron Adler, Ph.D., J.D.
8011 Candle Lane
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; PUBLICATION INFORMATION: US-08-377-522C-1
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TELEFAX: (713) 777-6908
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
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NAME: Benjamin Aaron Adler, Ph.D.,
NAME: 35,423
Real 9
Real 9
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LIBRARY: (FIXI; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: FIX1, FIX POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                             767 agagaatgcccatataccatccttcttttttgtgtctattagatgctca 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                      1007 ccaaacaggctccagaagaaatgtcaactgagaggaagcctgaaggatgaacagtgggc 1066
                                                                                                                                                                                                                                                                 127 AAGGTGGAACAGAGACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAG 186
                                                                                                                                Local Similarity
                                                                                     247 CCAAACAGGCTCCAGAAGAAATGTCAACTGAGGAAGCCCTGAAGGATGAACAGTGGGC 306
1247 cottotgtaaaattoatgotaaactacotaagagotatotacogttocaaagcaatagtg 1306
                                                                                                                                                                          307 TAAGCAAAGGGTTATTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAAGAGAG 366
                                                                                                                                                                                                                                                                                                                                                                                                   7 ACAGAGATGCCCTATACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCA 66
                                           487 CCTTCTGTAAAATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTG 546
                                                                                                                                                                                                                                                                                                                       aaggtggaacagagacaagcctatcaacacctacaagactggtggtaagtgcagtgacag 946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.6%; Score 1372.8; DB 7; Length 1608; 99.4%; pred. No. 2.4e-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D5919
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Sequence 1, Application US/08377522D GENERAL INFORMATION:
                                                           ADDRESSEE: Benjamin Aa
STREET: 8011 Candle La
CITY: Houston
STATE: TX
ZIP: 77071
COUNTRY: USA
COMPUTER READABLE FORM:
                                                                                                                                                                                                               APPLICANT: Mountz et al.
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSE:
ADDRESSES:
                                                                                                                                                                                                                                                                                                                                                                                                                         1386 GCCTCTTCTCCCGCGG 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2147 gcctcttctcccgcgg 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2087 aggggggggcactggcacggaacaccactgaggccagccctggctgcccaggcggagct 2146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1266 GTTCAAAGACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTC 1325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTATGCGATTTGGCTTAAGTTGTTAGCTTTGTTTTCCTCTTGAGAAATAAAAACTAAG 726
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                                                                                                                                                       E: Benjamin Aaron Adler, Ph.D., J.D.
8011 Candle Lane
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                  1127 ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                367 TTCCAGAGTGAGGTGCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placental
IMMEDIATE SOURCE:
LIBRARY: (FIXII; EMBL-SP6/T7
CLONE: FIXI, FIX2, FIX3; EMBL1
                                                                                                                                                                                                                                                      187 ATGCAAAACACAGGGTGATGGAAAGCCCTCAGGAGGGTAACCTAAGCTAGATTTGAGGGC 246
                                                                                                                                                                                                                                                                               947 atgcaaaacacagggtgatggaaagccctcaggagggtaacctaacctagatttgagggc 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                       67 GAGTGTGTGCACAAGGCTGGCACGCCCAGGGTCTTCCTCATGGCACTAACAGTCTACTGA 126
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DESCRIPTION: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 48.6%; Score 1372.8; DB 7; Length 1608; Local Similarity 99.4%; Pred. No. 2.4e-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: doubl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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US-08-377-522D-1

APPLICANT:

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US-60-324-185-29531
US-60-324-185-29531, Application US/60324185
Sequence 29531, Application US/60324185
GENERAL INFORMATION:
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                                                                                                                             847
                                                                   1266 GTTCAAAGACGCTTCTGGGGAGTGAGGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTC 1325
                                       2147
                             1386 GCCTCTTCTCCCGCGG 1401
                                                                                                                                                                                                                                                                                                                                 GGCCAGGAATAATGAGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGG 666
                                                                                                                                                                                                                                                                                                ggccaggaaataatgagtaacgaaggacaggaagtaattgtgaatgtttaatatagctgg 1426
                                                                                                                                                                                                                                                  ggcaggacctctgcgctctgagctccattctccttcaagacctccccaacttcccaggtt 1726
                                                                                                                                                  GTGAG-ATGCCAGCCACTGCAGGAACGCCCCGGGACAGGAATGCCCATTTGTGCAACGAA 1085
                                                                                                                                                       GAACTACAGCAGAAGCCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAA 1026
                                                                                                          gcctcttctcccgcgg 2162
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 415714.1
US-60-324-185-29531
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APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
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LENGTH: 3814
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CURRENT APPLICATION NUMBER: US/60/324,185
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL PROGRAM
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les 717; Conserva
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                                                                                                                                                                        1926
                                                                                                                                                                                                           1866 ctgacttctccccttccctacccgcgcgcaggccaagttgctgaatcaatggagccctcc 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ccctatggcgcaacatctgtactttttcatatggttaactgtccattccaggaacgtctg 120
                                                                                                                                                                                                                                                  361
                                                                                                           1986 gtgagotogtototgatotogogoaagagtgacacacaggtgttcaaagacgcttotggg 2045
          2105 ggaacacaccctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgg 2162
                                                           421 ctgacttctcccccttccctacccgcgcgcaggccaagttgctgaatcaatggagccctcc 480
                                                                                                                                              481 ccaaccegggegttecceagegaggettectteccatectectgaccaccggggettttc 540
                                                                                              541 gtgagetegtetetgatetegegeaagagtgacacaeggtgtteaaagaegettetggg 600
                                               tgagcctctcatgttgcagccacaacatggacagcccagtcaaatgccccgcaagtcttt 180
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ggaacacaccctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgg 718
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: U5/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
NUMBER OF SEQ ID NOS: 32
                 2813 aatcaaagagacgtg 2827
                                                            2753 aaacttgagcagcctgttttgaaaagtccctcgctcagaaatgccagcttgcagatggct 2812
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                                                                                                                           2693 tgctggggttggtggtactcgttcccaccgcacagaacccggcgcctattattggccaag 2752
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706 aatcaaagagacgtg 720
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                                                                                                                                                                                           2633 ctctttctttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcc 2692
                                            646 aaactigagcagcctgttttgaaaagtccctcgctcagaaatgccagcttgcagatggct 705
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                                                                                                          586 tgctggggttggtggtactcgttcccaccgcacagaacccggcgcctattattggccaag 645
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                                                                                                                                                                                                                                         466 ctctttaagactgtaagtcgctgcctgagtggtttcattttgtttttgtttttctgccctt 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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Sequence 674, Application US/09524038
GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark C.
APPLICANT: Dones, Lee w.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REPERENCE: 780CIP
CURRENT APPLICATION NUMBER: US/09/524,038
CARLIER APPLICATION NUMBER: 09/404,284
EARLIER APPLICATION NUMBER: 09/404,284
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TYPE: DNA
ORGANISM: Homo sapiens
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; Sequence 14682, Application US/09306350A

; GENERAL INFORMATION:
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SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 674
                                                    US-09-306-350A-14682
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Best Local Similarity 99.3%;
                                                                                            APPLICANT: Jones, Lee W.

APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Novel Nucleic Acid Sequences Óbtained
TITLE OF INVENTION: From Various cDNA Libraries
TILE REFERENCE: 20411-776
CURRENT APPLICATION NUMBER: US/09/306,350A
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 41304
SOFTWARE: pt_CT_1 Version 1.1
SEQ ID NO 14682
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                   Query Match
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       Y Match 11.3%;
Local Similarity 96.3%;
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391;
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 0; Mismatches
          Score 319.6; DB 17; pred. No. 9.1e-59;
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SEQ ID NO 14682
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                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/909,629
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/306,350
PRIOR FILING DATE: 1999-05-07
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                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 458
                                                           1021 gaagaaaatgtcaactgagaggaagcctgaaggatgaacagtgggctaagcaaagggtta 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 TCACCAGAGCACGAAAGAATTACAAGATTTTTTTTTCTCGTGCCGATT 58
              1141 gcagagettggtggacgatgccaaaggaatactgaaacetttagtgtgtccagtctggaa 1200
                                                                                                                                                                                 280 GCAGAGCTTGGTGGGCGATGCCAAAGGAATACTGAAACCTTTAG-GTGTCCAGTCTGGAA 222
                                                                                                                                                                                                                                                          Match 11.3%; Score 319.6; DB 34; Length 458; Local Similarity 96.3%; Pred. No. 9.1e-59;
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                                                                                                                                                                                                                                                 391; Conservative
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Labat, Ivan
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

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6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

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Copyright (c) 1993 - 2000 Compugen Ltd.
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PCT-US02-25766-9394
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US-10-13-872-1669
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US-10-175-523-103
US-10-027-632-253750
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US-10-027-632-253750
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                                                                                                                                                                                           Sequence 1262, Ap
Sequence 674, App
Sequence 477, App
Sequence 21, App1
Sequence 85, App1
Sequence 9394, Ap
Sequence 1263, Ap
Sequence 1263, Ap
Sequence 1259, Ap
Sequence 1259, Ap
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         Sequence 253751,
Sequence 64316,
                                    134015,
134016,
10281, A
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103, App
103, App
2303, App
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91808, A
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ore 2370.4; DB 6; ed. No. 0; Mismatches 21; 1 aaataaaaataacctttaga agatttcattcaatagatti ggtgttcattcaatagatti ggtgtttcattcaatagatti [	US-10-035-832-1262 US-10-035-832-1262 Sequence 1262, Application US/10035832 Sequence 1262, Application US/10035832 Sequence 1262, Application US/10035832 Sequence 1262, Application Investice Applicant: Engelhard, Eric TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR OFFILE REFERENCE: A-71249/ENS/DCF FILE REFERENCE: A-71249/ENS/DCF CURRENT APPLICATION NUMBER: US/10/035,832 CURRENT FILING DATE: 2002-07-22 CURRENT FILING DATE: 2002-12-22 PRIOR APPLICATION NUMBER: US 09/747,377 PRIOR FILING DATE: 2001-03-02 PRIOR FILING DATE: 2001-03-02 PRIOR FILING DATE: 2001-03-02 PRIOR FILING DATE: 2001-03-02 SOFTWARE: Patentin version 3.1 SEQ ID NO 1262 SEQ ID NO 1262 US-10-035-832-1262	US-10-027-632-264317 US-10-027-632-296990 US-10-027-632-296991 US-10-140-924-1 7 US-10-140-924-1 7 US-10-027-632-103140 PCT-US02-23268-3 US-10-027-632-71673 US-10-027-632-71673 US-10-035-832-1229 US-10-035-832-1229 US-10-035-832-1328 US-10-035-832-1328 US-10-035-832-1328 US-10-035-832-1328 US-10-035-832-1328 US-10-035-832-1328 US-10-035-832-1328 US-10-035-832-1328 PCT-US02-09188-1404 PCT-US02-09188-1404 PCT-US02-09188-1404 PCT-US02-09257-786 PCT-US02-09257-786
DB 6; Length 45121; 21; Indels 393; Gaps	CANCER	Sequence 64317, A Sequence 296990, Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1296, Ap Sequence 1217, App Sequence 1229, Ap Sequence 1239, App Sequence 1128, Ap Sequence 11688, Ap Sequence 1328, Ap Sequence 1328, Ap Sequence 1328, Ap Sequence 1402, Ap Sequence 1404, Ap Sequence 786, App

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL NUCLEIC ACID Sequences Obtained TITLE OF INVENTION: From Various Libraries

FILE REFERENCE: 780CIP
FILE REFERENCE: 780CIP
CURRENT APPLICATION NUMBER: US/10/011,154

CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/524,038
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-13
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/404,284
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/404,284
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
                                                                                                                                                                                                                                     APPLICANT: Drmanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birg
APPLICANT: Dickson, Mark C.
APPLICANT: Jones, Lee W.
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                                 SEQ ID NO 674
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TYPE: DNA
           LENGTH: 449
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                                              PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/214,886

PRIOR APPLICATION NUMBER: 60/217,487

PRIOR APPLICATION NUMBER: 60/217,487

PRIOR FILING DATE: 2000-07-11

PRIOR FILING DATE: 2000-08-14

PRIOR FILING DATE: 2000-07-26

PRIOR APPLICATION NUMBER: 60/220,963

PRIOR APPLICATION NUMBER: 60/217,496

PRIOR FILING DATE: 2000-07-11

PRIOR PRIOR PRIOR DATE: 2000-07-11

PRIOR PRIOR PRIOR DATE: 2000-08-14

PRIOR PRIOR PRIOR DATE: 2000-08-14

PRIOR PRIOR APPLICATION NUMBER: 60/225,447

PRIOR PRIOR PRIOR DATE: 2000-08-14

PRIOR PRIOR PRIOR DATE: 2000-08-14

PRIOR PRIOR PRIOR DATE: 2000-07-16

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CURRENT FILING DATE: 2002-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: PJZ16C1N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/760,486
PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1860 ctcaccctgacttctcccctccctacccgcgcgcgcgaggccaagttgctgaatcaatggag 1919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 1778 SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 CTCACCCTGACTTCTCCCCCCCCCCCCCCCGCGCGCGCAGGCCAAGTTGCTGAATCAATGGAG 210
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Local Similarity 99.3%;
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Pred. No. 4.5e-81;
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, OTHER INFORMATION: n equals a,t,g, or c US-10-143-906-21
        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     SEQ ID NO 21
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                                                                                                                                       OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ70C1N
CURRENT APPLICATION NUMBER: US/10/143,906
CURRENT FILING DATE: 2002-05-14
                                                                                                 NAME/KEY: misc_feature LOCATION: (704)
                                                                                                                                                                                                                                                                                                                                     Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID_NOS: 96
                                                                                                                                                                                                   OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                              LOCATION: (594
                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: (593)
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LENGTH: 772
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OTHER INFORMATION: n equals a,t,g, or c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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                                                                                                                                                                                                                                                                                                        772
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        8.4%;
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Score 237.4; DB 7;
Pred. No. 5.1e-41;
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         Length 772;
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Sequence 9394, Application PC/TUS0225766
GENERAL INFORMATION:
APPLICANT: GENE LOGIC, INC.
APPLICANT: MUNGER, William E
APPLICANT: FAULK, Ronald
APPLICANT: SUN, Hongwei
APPLICANT: SASAI, Hitoshi
APPLICANT: WAGA, Iwao
APPLICANT: YAMAMOTO, Jun
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 85
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo sapiens
APPLICANT: FAULE, APPLICANT: SUN, Hongwei APPLICANT: SASAI, Hitoshi APPLICANT: SASAI, Hitoshi APPLICANT: WAGA, Iwao APPLICANT: WAGA, Iwao APPLICANT: YAMAMOTO, Jun TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases FILE REFERENCE: 44921-5068-90.
CURRENT APPLICATION NUMBER: PCT/US02/25766
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Sequence 85, Application PC/TUS0210824

GENERAL INFORMATION:

APPLICANT: OriGene Technologies

TITLE OF INVENTION: Prostate Cancer Expression Profiles

FILE REFERENCE: 9U 206 PCT

FILE REFERENCE: 9U 206 PCT/US02/10824
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CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/281,732
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/281,731
PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                           2128 tggctgcccaggcggagctgcctcttctcccgcgg 2162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2551;
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APPLICANT: FOLLAY, ETIC
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF ESO ID NOS: 1613
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1263
LENGTH: 2551
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SEQ ID NO 9394
LENGTH: 2551
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; Sequence 143, Application US/10007926A
                                             US-10-007-926A-143
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PRIOR FILING DATE: 2001-08-14
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                                                                                                                                                                                                   tggctgcccaggcggagctgcctcttctcccgcgg 155
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APPLICANT: BERTUCCI,
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                                                                                                                                                                                                                                          US-09-053-375B-233
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PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: APPLICANT:
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                                                                                                                                                   Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/053,375B CURRENT FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                               TIPLE OF INVENTION: Nucleic Acid Arrays FILE REFERENCE: CLON-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chenchik, Alex APPLICANT: Bibilashvilli, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: tumor necrosis factor receptor superfamily, OTHER INFORMATION: member 6 (TNFRSF6) gene.
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                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                              LENGTH: 2534
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2034 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y Match 5.5%; Score 155; DB 7;
Local Similarity 100.0%; Pred. No. 3.1e-23;
hes 155; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
61 ggcactggcacggaacacccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                       1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOULGATTE, KERLA
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                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRANCOIS
                                                                                                                                                       4.6%; Score 129; DB 5; Length 2534;
100.0%; Pred. No. 1.1e-17;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2551;
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                                                                                                                                                                     0; Gaps
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2154 ctcccgcgg 2162

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CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTMARE: Patentin version 3.1
SEQ ID NO 1259
                                                                                                                                                                                    Matches 152; Conserv
                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-035-832-1259
                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (55549)..(55568)
OTHER INFORMATION: "n" at positions 55549 thru 55568 can be any base
                       Sequence 1259, Application US/10035832 GENERAL INFORMATION:
7799 cagtaaagaagtataagaattttttttaacgaaaattggtcaggaaataatccgtaacaa 7858
                                                                               1272 acctaagagctatctaccgttccaaagcaatagtgactttgaacagtgttcacca--gag 1329
                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (53136)..(53155)
OTHER INFORMATION: "n" at positions 53136 thru 53155 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1259,
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (53136)..(53
                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (50692)..(50711)
OTHER INFORMATION: "n" at positions 50692 thru 50711 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (48271)..(48290)
OTHER INFORMATION: "n" at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Engelhard, Eric
TITLE OF INVENTION: MOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (50692)..(507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (469\overline{8}7)...(47006) OTHER INFORMATION: "n" at positons 46987 thru 47006 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: (46987)...(47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (42691)..(42710)
OTHER INFORMATION: "n" at positions 42691 thru 42710 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: (42691)..(42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (31023)..(31239)
OTHER INFORMATION: "n" at 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (29253)..(29272)
OTHER INFORMATION: "n" at positions 29253 thru 29272 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Morris, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                               2.4%; 63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at positions 48271 thru 48290 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at positions 31023 thru 31239 can be any base
                                                                                                                                                                           0; Mismatches
                                                                                                                                                                Score 68.2; DB 6; Length 55996;
Pred. No. 0.00028;
0; Mismatches 83; Indels 4;
                                                                                                                                                                4; Gaps
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APPLICANT:
APPLICANT:

Vedvick, Thomas S. Kalos, Michael D. Sleath, Paul R. Carter, Darrick

Robert A.

APPLICANT:

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121,478C19
CURRENT APPLICATION NUMBER: US/10/113,872
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 2011

SOFTWARE: FastSEQ for Windows Version 4.0

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US-10-113-872-796/c
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CURRENT FILLING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1099-11-23
                                                             Sequence 796, Application US/10113872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-027-632-145670/c
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert,
APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 145670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                      247 AAGATAGTACAGAAAATTCCCACATACTGCACACCGTTTCCCCCTGTTTTAACATTTTAT 188
                                                                                                                                                                                               757 gagataatacagagaatgcccattataccatccttccttatcccacttctttttgtgtctat 816
                                                                                                                                                                                                                                                        697 tttttttatttaaatgaacttttcattttggaatagttttaggatttcaaaaaatttgca 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7859 aag-gaggaagtaataatgtet-aacacageaggtgagggtttteeettttaetgaaaat 7916
                                                                                                                                                                                                                                                                                                                                                          83;
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                                                                                                                                                                                                                                                                                                                                                                        2.2%;
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                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Score 60.8; DB 7
Pred. No. 0.0033;
                                                                                                                                                                                                                                                                                                                                                                                     DB 7; Length 816;
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-10-113-872-796
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Sequence 91808, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,066
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                    US-10-027-632-91808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Franger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF SECURITION NUMBER: US/10/113,872
CURRENT FILING DATE: 2002-03-28
NUMBER OF SECURITION WINDOWS VERSION 4.0
SECURITION 1569
LENGTH: 2821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Watanabe, Yoshihiro APPLICANT: Henderson, Robert !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2319 TAGATTTACAGAGAAGTTGCAGAGATAGTACAAAGAGTTCCTGTATACCCTTCACC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            676 ttttccttccttcttttacattttttatttaaatgaacttttcattttggaatagtt 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            736 taggatttcaaaaaatttgcagagataatacagagaaatgcccatataccatcc 791
                                                                                                                                                                                                                                                                                                                                                                         Match 2.1%; Score 60; DB 7; Length 2435; Local Similarity 69.8%; Pred. No. 0.0067; Length 2435; Local Similarity 69.8%; Pred. No. 0.0067; Local Similarity 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676 tittccttccttcttttacattttttatttaaatgaacttttcattttggaatagttt 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Indels 0; Gaps
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 91808
LENGTH: 542
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR ETLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-304597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence General Information: General General Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome TITLE OF INVENTION: Polymorphisms in the Human Genome TITLE OF INVENTION: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 79.5%;
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
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PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 304597
LENGTH: 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                  Matches
                                                                                                                                          Query Match
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PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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watch 2.1%; Score 59.2; DB 7; Length 542; Local Similarity 79.5%; Pred. No. 0.0066; les 70; Conservative 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10027632
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Pred. No. 0.0066;
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757 gagataatacagagaatgcccatatacc 784

Db 104 gagataatacaaaagttccttcacacc 131

Search completed: September 8, 2002, 01:14:46 Job time: 37364 sec

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OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                           Score
286.4
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                       AA05863 zf5504.s

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H86126 ys94g08.s1

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AV715411 AV715411
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BI763679 603049567
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zj19h02.sl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:450771 3', mRNA sequence.
AA704610 .....
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                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 467)
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                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
                                                                                                                                                       Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                      Fax: 314 286 1810
                                                                                                                                          High quality sequence stop: 459.
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932
1052
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1101
506
                 /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
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/sex="male"
                                                                           /db_xref="taxon:9606"
/clone="IMAGE:450771"
                                                                                                 /organism="Homo sapiens"
/db_xref="GDB:1387127"
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AL063921 Drosophil
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BI045052 MR4-OT019
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AL108811 Drosophil
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BG978282 RC4-G1019
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                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcagagataatacagagaatgcccatataccatcctccttatcccacttcttttgtgtc 813
                                       Tissue Procurement: Life Technologies, Inc
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 793)
                                                                                                                                                                               Homo sapiens
       CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                  603049567F1 NTH_MGC_116 Homo Sapiens cDNA clone IMAGE:5189752 5
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Sequencing by: Incyte Genomics, Inc.
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                               215504.51 Soares retina N2b4HR Homo sapiens cDNA clone NAOKSE380815 3', mRNA sequence.
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/clone="IMAGE:5189752"
/clone_lib="NIH_MGC_116"
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 2768 gttttgaaaagtccctcgctcagaaatgccagcttgcagatggctaatcaaagagacgtg 2827
                                                                                                            121 CCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGG 180
                                                                                                                                                                                                                                                      Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, M., Hulman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohifing, T., B., Morris, M., Parsons, J., Prange, C., Thierny-Meg, J., Trevaskis, E., Schellenberg, K., Soares, M.B., Tan, F., Thierny-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Genome Res. 6 (9), 807-828 (1996)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                      Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 467.
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Local Similarity
                                                                                                                                                                  AA056275 577 bp mRNA linear EST zf53g03.sl Soares retina N2b4HR Homo sapiens cDNA clone
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                               Conservative
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/lab.host="pH105 (ampicillin resistant)"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
/note="lorgan: eye; Vector: pT7T3D (Pharmacia) with a
/note="lorgan: eye; Vector: pT7T3D (Pharmacia) with a
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/db_xref="GDB:1288949"
/db_xref="taxon:9606"
/clone="IMAGE:380692"
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Fax: 314 286 1810
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The WashU-Merck EST Project
Unpublished (1995)
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1 (bases 1 to 442)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 372
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TMAGE:360867 3', mRNA sequence.

AA011026
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                                                                                                                                                        University of Toronto. Soares and M.Fatima Bonaldo.
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/dev_stage="55 year old"
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                10.1%;
Score 286.4; DB 9
Pred. No. 1.1e-41;
                           DB 9;
                                                                                                                                              2 others
                       Length 442;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, S., B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Scares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M., Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 547)
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                                                                                                                                                                                                                                                                                                                                                                              Forest Park Parkway, Box 8501, St. Louis, MO 63108
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1
                                                                                                  /clone_lib="Soares retina N2b4HR"
/sex="male"
                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:380300"
                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:1288557"
                                                                                                                                                                                                                              ocation/Qualifiers
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1 (bases 1 to 447)

1 (bases 1 to 447)

1 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman Hillier, L., Clark, N., Dubuque, T., Elliston, K., Marra, M., Parsons, J., M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., M., Rohlifing, T., Soares, M., Tan, Fi., Trevaskis, E., Waterston Rifkin, L., Rohlifing, T., Wohldmann, P. and Wilson, R. The Washu-Merck EST Project
The Washu-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                            AA057418 447 bp mRNA linear EST 2f59h03.s1 Soares retina N2b4HR Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                  AA057418.1 GI:1550059
                                                                                                                                                                                                                                                                                                                                                                                                                  IMAGE:381269 3', mRNA sequence.
                                                                                                                                                                                     Unpublished (1995)
Contact: Wilson RK
                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 339.
                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. | Louis, MO 63108
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/db_xref="GDB:1289526"
            /organism="Homo sapiens"
                                          Location/Qualifiers
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Pred. No. 1.1e-41;
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467 bp mRNA linear EST 30-JAN-1990 AA020992
ze65f07.sl Soares retina N2b4HR Homo sapiens cDNA clone ze65f07.sl Soares retina N2b4HR Homo sapiens cDNA clone ze65f07.sl Soares retina N2b4HR Homo sapiens cDNA clone
1 (bases 1 to 467)
Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Gish, W., Hawkins
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Mardis, E., Moore
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E.,
M., Hultman, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                                                                                                                                                          AA020992.1 GI:1484745
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/clone="IMAGE:381269"
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/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
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                                                                                                                                            2708 tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct 2767
                                                                                                                                                                                       2648 ccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctggggttggtgg 2707
                                                                                                                                   182 TACTCGTTCCCACCGCACAGAACCCCGGCGCGCTATTATTGGGCCAAGAAACTTGAGCAGCCT 241
                                                                                                                                                                                                                               242 GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCA 279
                                                                                                                                                                          122 CCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGG 181
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                        376 bp mRNA linear EST IMAGE:222568 3', mRNA sequence.
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Seq primer: -40M13 fwd. from Amersham
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/dev_stage="55 year old"
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:363877"
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/db_xref="GDB:1280580"
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
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High quality sequence stops: 364
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: Promega -21m13
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1 (bases 1 to 376)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., R., Williamson, A., Wohldmann, P. and Wilson, R., Washu-merck EST project

The Washu-merck EST project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old hrs after their removal. The retina RNA was extracted 6 provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Organism="Homo sapiens"
/db_xref="GDB:3851329"
/db_xref="taxon:9606"
/clone="!MAGE:222568"
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/dev_stage="55_year_old"
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1 (bases 1 to 398)
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ys94g08.s1 Soares retina N2b5HR Homo sapiens cDNA clone
IMAGE 222494 3', mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Source: IMAGE Consortium, LLNL Source: IMAGE Consortium, LLNL Free through LLNL; contact the This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.lnl.00)
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Location/Qualifiers
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High quality sequence stops: 378
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314 286 1810
                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GDB:3851255"
/db_xref="taxon:9606"
/clone="IMAGE:222494"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 297)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA018441.1 GI:1481696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
See primer: -40M13 fwd. from Amersham
High quality sequence stop: 244.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                     59
    double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector the PATTA control of the retinas were obtained from a 55 year old (Pharmacia). The retinas were obtained from a 55 year old caucasian and total cellular poly(A)+ RNA was extracted 6 caucasian and total cellular poly(A)+ RNA was kindly hrs after their removal. The retina RNA was kindly hrs after their removal. The retina RNA was with the provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                  /tisue_type="retina"
/dey_stage="55 year old"
/dey_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: estiwatson.wustl.edu
High quality sequence stops: 361
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
INSERT Length: 882 Std Error: 0.00
Seq primer: Promega -21m13
Seq primer: Promega -21m13
Location/Qualifiers
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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IMAGE:223321 3', mRNA sequence.
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/lab_host="DH10B (ampicillin resistant)"
//note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
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                                                                                                                                                                                                                                   /dev_stage="55 year old"
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    Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 958 Std Error: 0.00 Seq primer: Promega -21m13
High quality sequence stop: 269
                                                                                    Email: est@watson.wustl.edu
Insert Size: 958
High quality sequence stops: 269
                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                   Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                      Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                  ,R., Williamson,A.,
The WashU-Merck EST
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1 (bases 1 to 419)
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y922910.s1 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:274746 3', mRNA sequence.
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Soares and M.Fatima Bonaldo.
a 90 c 101 g 116 t
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AV715411
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                           Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
251 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                           Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 696)
                                                                                                                                                                                                                                                                                         ,G., Cheng,Z. and Han,Z.
Homo sapiens cDNA DCB clones
                                                                                                                                                                                                                                                  Unpublished (2000)
Email: hanzg@chgc.sh.cn
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Soares and M.Fatima Bonaldo. "

104 g 117 t 6 others
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/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a /note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st modified polylinker; Site_1 in oligo(dT) primer [5′ strand cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primed with a Not I - oligo(dT) primer [5′ retractant cDNA was primer [5′ retractant cDNA was primer [5′ retractant cDNA was primer [5′ r
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                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11560 row: f column: 19
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                           National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                     High quality sequence stop: 813.
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/dev_stage="mature"
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/note-"Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo
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/clone="IMAGE:5222802"
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                                              /lab_host="DH10B"
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2586 taagtcgctgcctgagtggtttcattttgtttttgtttttcttgccc 2630
                                                                                          253 a
                                                                                                                                                                                                                                                                                                   male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
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Search completed: September 7, 2002, 14:51:57 Job time: 16216 sec

181 TICTTACGTCTGTTGCTAGATTATCGTCCAAAAGTGTTAATGCCC 225

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OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
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## ALIGNMENTS

/db/xref="taxon:9606" ASE COUNT 579 a 595 c 568 g 638 t RIGIN	EATURES Location/Qualifiers  source /organism="Homo sapiens"	substances potentially useful for convey control patent: DE 19847779-C 3 03-FEB-2000; DENTESCHES KEEBSFORSCH (DE)		Eukaryota; Metazua, Cibruca, Catarrhini; Hominidae; Homo Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (hases 1 to 2380)	ORGANISM Homo sapiens ORGANISM Homo sapiens	S	CESSION AX026091 PRSION AX026091.1 GI:10187522	AX026091 2380 DP DWG ON Sequence 3 from Patent DE19847779.	91	
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		•	modulating ,v	Homo.	Euteleostomi;			!	PAT 16-SEP-2000	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1801 agagaggagcggaactcctggacaagccctgacaagccaaagccaaaggtccgctccggcg 1860
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                                                                                                                                                                                                                                             CCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTTCCCACCGCACAG 2727
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                                                                                                                                                                                                                                                                                                       CATTITIGITITGTTTTTCTGCCCTTCTCTTTCTTCTTTTGCCCCTTTCTTAGCTTGCACTC
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       AL157394.15 GI:15384622
                                                  Human DNA sequence from clone
                                                                    AL157394
                            PRI 22-AUG-2001
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Db 142476 GGCTATAATGATAAGTATTAAGTAAGGAAGATCCACATATGTGAGTTGCTGGCTTATAAT 142535
                                                                                                                                                                                                                                                     Db 142416 ACCTTTTTTGGCTACATTTTTTTATTTGTAAAGTAAGTTTAATAATCACTCATCTCACTG 142475
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following in the feature table with their source databases: Em:, EMBL; Sw;, Switssey, Smitssey, Switssey, Switssey, Emergine as the submission one submission one statement was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following in the feature table with their source databases: Em:, EMBL; Sw;, Switssey, Swit
This sequence is the entire insert of clone RP11-399019 The true left end of clone RP11-496H23 is at 166408 in this sequence. The true right end of clone RP11-304I5 is at 18704 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/Chr10
RP11-399019 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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           144876 ACCGTTTTTTATTGTCACACAGAAAAAGAAACTGCCTTGTCTCCCGTTCCGGGAATTCTCT 144935
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                                                                                        99ctataatgataagtattaagtaaggaagatocacatatgtgagttgctggcttataat 120
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1 (bases 1 to 3212)

Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy

Patent: DE 19847779-C 1 03-FEB-2000;

DEUTSCHES KREBSFORSCH (DE)
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                                                                         1141 caacatggacagccagtcaaatgccccgcaagtctttctctgagtgactccagcaatta 1200
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1948 cagacgtaggaaataagtcagcaccgaagcagtggttaagccggagggctcggaagaacg 2007
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                                                                                                                                                                                                                                                                                                                  Rudert, F., Visser, E., Forbes, L., Lindridge, E., Wang, Y. and
                                                                                                                                                                                       Submitted (26-MAY-1995) F.H. Rudert, Genesis Research Development, Corporation Ltd., PO Box 50, Auckland, NE Overlaps with x81335, & x82279-X82286.
                                                                                                                                                                                                                                                                                                           Watson,J
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Cell Biol. 14 (11), 931-937 (1995)
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                                                                                       /map="q24.
564. .133
        /note="lysozyme silencer 1"
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                                         /note="beta interferon silencer B motifs" complement(1237. .1244)
                                                                                                  /tissue_type="placenta"
/map="q24.1"
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/note="basal promoter"
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Local Similarity 100.0%; P
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Direct Submission
          Vakanishi, Y.
                              factor for interleukin-6 expression upon in
J. Biol. Chem. 270 (30), 18007-18012 (1995)
95355401
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2165)
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                                               Transcription stimulation of the Fas-encoding gene by nuclear
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                                                                  Wada.N., Matsumura,M., Ohba,Y., Kobayashi,N., Takizawa,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                          Homo sapiens blood DNA, clone pF7.
                                                                                                                                         Fas antigen.
                                                                                                                                                  D31968.1 GI:961455
                                                                                                                                                               Human DNA for Fas antigen, promoter region.
                                                                                                                                                                                 HUMFAS
                                                                                                                                                                             2165 bp
                                                                                                                                                                            DNA
                                     influenza virus infection
                                                                                                                                                                          linear
                                                                                                                                                                    PRI 14-APR-2000
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Query Match Best Local Similarity 99.9%; Pred: No. 0; Best Local Similarity 99.9%; Pred: No. 0; Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1714; Conservative 1; Indels 1; Indels 0; Gaps 0; Mismatches 1; Indels 0; Gaps 1; Indels 1;	rt=1 rras antigen" rpas antigen" "GI:4433150" ion="MLGIWTLLPLV" 165 555 g 547 t	/bound_molety="NF-ILO 934. 940 /bound_molety="NP-1" 948. 955 /bound_molety="Ets" /bound_molety="NF-ILO 12981306 /bound_molety="NF-ILO 14361813 14361813 /roa1813	NH	JOURNAL Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:nakanaka@dbs.p.kanazawa-u.ac.jp, Tel:076-234-4424, Fax:076-234-4480) Tel:076-234-4424, Fax:076-234-4480) FEATURES Location/Qualifiers 1. 2105 Source /organism="Homo sapiens"
WAAAACTAAGGGGCCCTCCCTTTCAGAGCCCTANGGCCTACGGCCAGCCAGCCAGCCTACGGCCCTACGGCCCTACGGCCCTACGGCCCTACGGCCCCCCCC	901 ttttttttaaagaaaattggccaggaaataatgagtaacgaaggacagac	ANTACTGANACCTTTAGTGTGTCCAGTCTGANACTTCAGG ANTACTGANACCTTTAGTGTGTGTCCAGTCTGANACTGCATCCANATTCAGG ANTACTGANACCTTTAGTGTGTCCAGTCTGTANACTAGCTAA  atgtcattatccaaagataccttctgtanaattcatgctanacctac	601 tgaaggatgaacagtgggctaagcaaagggttattaatgtgtttattaatgggttgaatct ood tgaaggatgaacagtgggctaagcaaagggttattaatgtgttattaatgggttgaatct ood tgaaggatgaacagtgggctaagcaaagggttattaatgagttallllllllll	CAAGACTG 48 pagggtaac 5- pagggtaac 5- pagggtaac 5- pagggaagcc 6- paggaagcc 7- pagga

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442 CGCGCGAGCCAAGTTGCTGAATCAATGGAGCCCTCCCCAACCCGGGCGTTCCCCAGCG	
1382 TGCCCAIIIGE	
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TCGAGGTCCTCACCTGAAGTGAGCGATGCCAGCCAGCCAG	
1321 ctcgaggtcctcacctgaagtgagcatgccaggcactgcaggaacgccccgggacCaGgaACAGGAACACCCCCGGGGACAGGAA 138	^
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662 AATTGGGAAGGGAGAGAGGAGAGGTAGCAGGTCTGGGAGCTCCGAGGTCCGGGTCGGTGGT	Вb
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Submitted (03-SEP-1994) P.H. Krammer, German Cancer Research
Center, Tumorimmunology Programm, Im Neuenheimer Feld 280, 69120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAAGAGTGACACAGATGTTCAAAGACGCTTCTGGGGAGTGAGGGAAGCCGGTTTACGA 1621
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Behrmann, I., Walczak, H. and Krammer, P.H.
Structure of the human APO-1 gene
Eur. J. Immunol. 24 (12), 3057-3062 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krammer, p
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join(1653. .1810)
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x81338.1:145. .253,x81339.1:552. .613,x81339.1:766. .828,
x81340.1:79. .161,x81341.1:255. .279,x81342.1:103. .1757)
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151. .261
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/chromosome="10"
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301 aaatttgcagagataatacagagaatgcccatataccatcctccttatcccacttcttt 360
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x81338.1:146. .253,x81339.1:552. .613,x81339.1:766. .828,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APO-1 gene;
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                                                                                                                                                                                                                                                                                                                      Submitted (20-OCT-1994) J. Cheng, Univ.of Alabama at Birmin Univ. of Alabama, 701 South 19th Street, UAB Station, LHRB Birmingham, AL 35294-0007, USA Related sequences: M07454 and X63717.
                                                                                                                                                                                                                                                                                                                                                                                                         J. Immunol. 154 (3), 1239-1245 (1995)
95123075
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1. (bases 1 to 1608)
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Olek,A., Piepenbrock,C. and Berlin,K.
Diagnosis of diseases associated with the immune
Patent: WO 0200928-A 2392 03-JAN-2002;
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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                                                                           1700 gcctcttctcccgcggacatgtaca 1724
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                                                             ggccaggaaataatgagtaacgaaggacaggaagtaattgtgaatgtttaatatagctgg 979
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Sequence 2391 from Patent WO0200928. AX347320
                 AX347320
                     1608 bp
                       PAT 01-FEB-2002
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1052 ttcagagccctatggcgcaacatctgtactttttcatatggttaactgtccattccagga 1111
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/db_xref="taxon:32630"
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 2 03-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9c9ctctgagctccattctccttcaagacctccccaacttcccaggttgaactacagcag 1291
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Sequence 2 from Patent DE19847779
AXO26090
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Mammalia; F
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      /organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match

Score 611.8;

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Length 720;

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Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: GTCTCCCTTCCGGGAATTCT
Primer B: AACCCCAGCAGGAGACCAA
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                                                                                                                                     Contact: Michael Olivier, David R. Cox
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Olivier, M. and Cox, D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)
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                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                      398 bp DNA linear STS 30-MAR-2
SHGC-30908 Human Homo sapiens STS genomic, sequence tagged site.
G27038
                                                                                                                                                                                                                                                                                                                                  G27038.1 GI:1375288
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                                                                                      CA 94025, USA
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                                                                                                         RESULT 13
           SOURCE
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                                                                                                BC012479
                                          ACCESSION
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ORGANISM
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                                                                                                                                                                                                                                                                                      2166 tgttttgtttttctgcccttctctttctttttgccctttcttagcttgcactcccatg 2225
                                                                                                                                                                                                                                                                                                                      2226 gtgatttctgcttggtctcctgctggggttggtactcgttccccaccgcacagaaccc 2285
                                                                                                                                         121 GTGATTTCTGCTTGGTCTGCTGGGGTTGGTGGTACTCGTTCCCACCGCACAGAACCC 180
                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                             270; Conservative
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PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prepared with primer pairs provided by Sandoz, derived from H86126
-- Washington University/Merck EST sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buffer:
                                                               Homo sapiens, Similar to tumor necrosis factor receptor superfamily, member 6, clone MGC:21432 IMAGE:4514272, mRNA
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                     BC012479
 Homo sapiens
                                BC012479.1 GI:15214691
                                                       complete cds.
              numan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Human"
                                                                                                                                                                                                                                                                                                                                                                                10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      93 c
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Pred. No. 4.7e-56;
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Query Match
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                                                                                                                                                                                   61 GGCTTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACG 120
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 28 Row: i Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                    245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             superfamily, member 6"
/protein_id="AAH12479 1"
/db_xref="G1:15214692"
/translation="MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV
/translation="MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV
TTONLEGIHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCR
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SNTKCKEEGSRSNLGWLCLLLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNEE
TVAINLSDVDLSKYITTIAGVWTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="pladder, transitional cell papilloma"
/clone_lib="NIH_MGC_93"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="MGC:21432 IMAGE:4514272"
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superfamily, member 6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532 c
                                                                                                                                                                                                                                                                                                                                                                         10.3%; Score 245; DB 9; LengLu 2/2
100.0%; Pred. No. 2.6e-52; Indels
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         Ouery Match 9.1%; Score 216; DB 9; Length 702; Best Local Similarity 100.0%; Pred. No. 7e-45; Matches 216; Conservative 0; Mismatches 0; Indels
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 702)

Muschen,M., Re,D., Brauninger,A., Wolf,J., Hansmann,M.L., Diehl,V.,
Kuppers,R. and Rajewsky,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muschen, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 702)
Muschen,M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences: D31968 X89101 AJ279012 AJ279013
                                                                                                                                             /number=1
                                                                                                                                                      /standard_name="Apo-1 Fas"
                                                                                                                                                                            /gene="CD95"
                                                                                                                                                                                                           /translation="MLGIWTLLPLV"
                                                                                                                                                                                                                           /protein_id="CAC35539.1"
/db_xref="GI:13539239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene=
<1. .3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="Reed-Sternberg cells"
/note="Hodgkin's disease tissue"
                                                                                                                                                                                                                                                            /product="CD95 antigen"
                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                            standard_name="Apo-1 Fas"
                                                                                                                                                                                                                                                                                                                     /gene="CD95"
                                                                                                                                                                                                                                                                                                                                               /standard_name="Apo-1 Fas"
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                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name="Apo-1 Fas'
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          Gaps
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HSA279012
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   intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CTGGCTGCCCAGGCGGAGCTGCCTCTTCTCCCGCGG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGGCACGGAACACACCCTGAGGCCAGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CGCAAGAGTGACACACGGTGTTCAAAGACGCTTCTGGGGAGTGAGGGAAGCGGTTTACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgcaagagtgacacacaggtgttcaaagacgcttctgggggagtgaggggaagcggtttacg 1619
                                                                                                                                                                                                                                                                                                                                                                                                        Related sequences: D31968 X89101 AJ279011 AJ279013
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 702)
Muschen,M., Re,D., Brauninger,A., Wolf,J., Hansmann,M.L., Diehl,V.,
Kuppers,R. and Rajewsky,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muschen,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                side-effect of the germinal center reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Somatic mutations of the CD95 gene in human B cells as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 702) Muschen, M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuppers, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ279012.1 GI:13539240
Apo-1 Fas; CD95 antigen; CD95 gene.
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/translation="MLGIWTLLPLV"
314. .>702
                             /product="CD95 antigen"
/protein_id="CAC35540.1"
/db_xref="GI:13539241"
                                                                                                                                       /standard_name="Apo-1 Fas"
282. .>313
                                                                            /codon_start=1
                                                                                               /standard_name="Apo-1 Fas'
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                                                                                                                                                                      /gene="CD95"
                                                                                                                                                                                                         /number=1
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                                                                                                                                                                                                                                                                                               /cell_type="Reed-Sternberg cells"
/note="Hodgkin's disease tissue-polymorphic allele (+275)"
                                                                                                                                                                                                                                          /gene="CD95"
                                                                                                                                                                                                                                                                             /gene=
                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                             "CD95"
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/gene="CD95"
//standard_name="Apo-1 Fas"
//number=1
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OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                              Result
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                                                                                                                                                                                                              1372.8
879.4
856.8
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                                                                                                                                                                               190.4
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                  Match
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                      Length DB
                                                                      1608
1608
1608
859
266
2551
2471
                                                                                                             AAT34162
ABL34419
ABL34418
AAC98177
AAZ88700
AAC61798
                                                                                 AAQ93879
                                              AAX24878
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                                              Human colon cancer
Human CD95 recepto
DNA encoding a hum
Fas-delta-TM CDNA.
Soluble Fas recept
                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                      Human
                                                                                                                                                                                                                                                                     Human immune syste
                                                                                                                                                                                                                                                                                                    Fas promoter regio
                       Human cell surface
                                                                                                                                                                                                                                      immune syste
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Probe #9089	ABA30623	22	562	2.1	51 51	4.4 4.5
<b>=</b> :	AAS29933	3 K		2.2	Ĺ	43
Human	AAS61449	2 4		2.2	۳	42
Human	ABA16909	22		2.2	51.2	41
Dullan	AAS01142	22		2.2	_	40
u.man	AAK74027	22		2.2	-	39
TUDINI	AAS46692	22		2.2	_	ω : <b>œ</b>
Human	AAK66590	22		2.2	_ !	ນ ( 7
Human	AAZ27725	20	556	2.2		ر د د
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Multile	AAF58432	22		2.2		ب ا د
Hullan	AAK70808	22	5484	N	52.6	ب 1
RECEIODEAS COMA SEN	AAZ86967	21	162450	N	52.8	0
Hullian	ABL32859	24		2.2	ا بی	9 0
Hullan	AAH77407	22		2.2	53.2	ک ه
Human	AAL07188	22		2.2	w.	27
NUCLEOCIAG SCHACES	AAA96417	21	10640	2 . 3	54	96
Hullian	AAI85367	22		2.3	4	) t
Human	8	24		2.3	4	24
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Human	ABA21471		3545	2.3	54.8	) t
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Murine	AAZ23892		6901	2.4	י ת	) t
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UNA	AAS98633			2.5	۰	, C
, n.c.	AAV20441			2.5	٥	17
Supt manner	AAF68854	22	435	2.5	5	16
Himan Sideri	AAT27557	17		2.6	62.6	15
9 2	AAT2/558	17	307	2.7	ω	14
Shirt		i œ	534	5.4	7.	13
	AAV32993	19	534	5.4	N	12
i i i	AAT16303	17	2534	5.4	129	11
Plasmid	29		534	5.4	129	0

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ALIGNMENTS

## AAT34162 XX XX AC AAT3 AC AAT3 XX PAS FAS XX RESULT AAT34162 standard; DNA; 1608 BP Fas gene promoter; apoptosis; ageing; autoimmune disease; r-cell senescence; ss. AAT34162; Fas promoter region. 22-OCT-1996 Homo sapiens L (first entry)

Key promoter

Location/Qualifiers

.1074

protein\_bind

/\*tag= a
/note= "Fas gene promoter region"
147..151

/function= GF1 transcription factor binding site

protein\_bind

168..174

protein\_bind

protein\_bind

/\*tag=

/\*tag= d /function= Myb transcription factor binding site /note= "claim 9" 349..353

/function= EBP20 transcription factor binding site 272...276

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Matches 1388;
                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                 defined as the Fas gene promoter region. This includes a number of transcription factor binding sites. A coding sequence for the N-terminal portion (AAR99471) of the Fas protein leader peptide is also included. The DNA segment was isolated from a human ras cDNA placental DNA library using a 32P-labeled segment of human ras cDNA corresponding to nt 23-346. It can be combined with a structural gene so that the gene is under the transcriptional control of the transcription factor binding sites. The promoter region can be used to regulate Fas gene expression, e.g. in tumour or immune cells, as a means of treating Fas-mediated apoptosis disorders such as
                                                                                                                                                             Sequence 1608 BP; 398 A; 421 C; 423 G; 366 T; 0 other;
380 gagtgtgtgcacaaggctggcacgcccagggtcttcctcatggcactaacagtctactga 439
                                             320 agagaatgcccatataccatcctccttatcccacttctttttgtgtctattagatgctca 379
                                                                                                                                                                                                malignancies and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Fig 2; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    Human Fas gene promoter region - used for heterologous protein expression and for developing products for treating Fas-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR99471.
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                                                                                                          Match 57.7%;
Local Similarity 99.4%;
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                                                                                                                                                                                                                                                                                                                                 DNA segment (AAT34162) has an isolated sequence region as the Fas gene promoter region. This includes a numb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koopman WJ,
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0377522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US00606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1479..1469
/product= Fas protein leader
1497..1608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function= NF-Y transcription factor binding site /note= "claim \theta" 621...626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function= CP2 transcription factor binding site
/note= "claim 6"
1075..1476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function= AP-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function= NF-Y transcription factor binding site
/note= "claim 8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune system associated gene SEQ ID NO: 2392.
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01-SEP-2000; 2000DE-1043826.
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                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, heurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/vlacerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
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                                                                                                                                                                                                                                                                                                                                 1340 gtgagcatgccagccactgcaggaacgccccgggacaggaatgcccatttgtgcaacgaa 1399
                                               1280 gaactacagcagaaggctttagaaagggcaggaggccggctctcgaggtcctcacctgaa 1339
                                                                                                                                                                                                                                                                        882 AAACCCTCCCTTTTCAAAACCCCTATAACGCAACATCTATACTTTTTCATATAATTAACTA 823
                                                                                         762 AAATACCCCGCAAATCTTTCTCTAAATAACTCCAACAATTAACCAAAACTCCTATACCCA
                                 ATRCARARCACARAATAATAARAAACCCTCAAAAAAATAACCTAACCTAAATTTAAAAAC 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atgcaaaacacagggtgatggaaagccctcaggagggtaacctaacctagatttgagggc 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ССАРАСЛАВСТССКАРАВЛАВАВАНТАТСРАСТВАВАВАВАВССТВАВАВАВТАВАСАВТАВАС 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccaaacaggctocagaagaaaatgtcaactgagaggaagcctgaaggatgaacagtgggc 619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTACAAAATAAAAACTTAATAAACGATACCAAAAAAATACTAAAACCTTTAATA 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg 739
                                                                                                                                                                                                                                                                                        gggcctcccttttcagagccctatggcgcaacatctgtactttttcatatggttaactg 1099
                                                                                                                                                                                                                                                                                                                                                            ggctatgcgatttggcttaagttgttagctttgttttcctcttgagaaataaaaactaag 1039
                                                                                                                                                                                                                                                                                                                                                                                            AACCAAAAATAATAAATAACGAAAAACAAAAAATAATTATAAATATTTAATATATAACTAA 943
                                                                                                                                                                                                                                                                                                                                                                                                              ggccaggaaataatgagtaacgaaggacaggaagtaattgtgaatgtttaatatagctgg
                                                                                                                                                                                                                TCCATTCCAAAAACGTCTATAAACCTCTCATATTACAACCACAAAATAAACAACCCAATC
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77.1%;
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                               Claim 1; SEQ ID NO 2391; 32pp + Sequence Listing; German
                                                                                                           Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; anemode de disease; arteriosclerosis; anaemia; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                        02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                        03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 2391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523 CCCTAACTCCTTCCTCACCCTAACTTCTCCCCCTCCCTACCCGCGCGCAAACCAAATTAC 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccotgactcottcotcaccotgacttctcccccttcctacccgcgcgcgcaggccaagttgc 1459
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Best Local
                 1172 agtotttototgagtgaotocagcaattagocaaggotoctgtacocaggoaggaootot 1231
                                                                                                                                                   1052 ttcagagccctatggcgcaacatctgtactttttcatatggttaactgtccattccagga 1111
859 agtttttttttgagtgattttagtaattagttaaggtttttgtatttaggtaggattttt
                                                                                                                                                                                                                   619 atgagtaacgaaggataggaagtaattgtgaatgtttaatatagttggggttatgcgatt
                                                                                                                                                                                                                                                                                     932 atgagtaacgaaggacaggaagtaattgtgaatgtttaatatagotggggctatgcgatt 991
                                                                                                                                                                                                                                                                                                                                                     499 tttatgitaaattatttaagagitatttatcgitttaaagtaatagigattitgaatagi 558
                                                                                                                                                                                                                                                                                                                                                                                                                     812 ttcatgctaaactacctaagagctatctaccgttccaaagcaatagtgactttgaacagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    752 aactgcatccaaattcaggttcagtaatgatgtcattatccaaacataccttctgtaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      692 gtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtgtgtccagtctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelo: leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 tagaagaaaatgttaattgagaggaagtttgaaggatgaatagtgggttaagtaaagggt 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572 cagaagaaaatgtcaactgagaggaagcctgaaggatgaacagtgggctaagcaaagggt 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1608 BP; 398 A; 51 C; 423 G; 736 T; 0 other;
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                                                                                     acytotytyagoeteteatyttycayceacaacatyyacayeecayteaaatyceceyea 1171
                                                                                                                                tttagagttttatggcgtaatatttgtatttttttatatggttaattgtttattttagga 798
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                                                                                                                                                                                                  gtttattagagtacgaaagaattataagatttttttttaaagaaattggttaggaaata
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76.7%;
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Pred. No. 5.7e-229;
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antigens, useful for the treatment, prevention, and diagnosis of colon

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; reproductive disorder; gastrointestinal disorder; renal disorder; medications disorder; renal disorder; respectives disorder; renal disorder; respectives disorder; renal disorder; respectives disorder; renal disorder; respectives disorder; renal disorder; renal disorder; respectives disorder; renal disorder; rena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer antigen nucleotide sequence SEQ ID NO:187.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infectious disease; cardiovascular disorder; ss.
Colon cancer associated gene sequences, \operatorname{referred}^{\!\scriptscriptstyle j} to as colon cancer
                                                                                                                                                                                                                                                                        12-MAR-1999;
                                                                                                                                                                                                                                                                                                                          08-MAR-2000; 2000WO-US05883.
                                                              P-PSDB; AAB53420
                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                   Rosen CA, Ruben SM;
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AAZ88700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, proteins and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, such as gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAD98764 to AAC98772 and AAD54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 610-611; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1508 cttcccatcctcctgaccaccggggcttttcgtgagctcgtctctgatctcgcgcaagag 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 859 BP; 214 A; 219 C; 227 G; 193 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1568 tgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacgagtgactt 1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                                                                                                                                                                                                                                                                                                                                                                           AAZ88700 standard; DNA; 266 BP.
                                                                                                                                                           protein_bind
                                                                                                                                                                                                                                             cancer chemotherapy; ss.
                                                                                                                                                                                                                                                         p53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                                                                                                           Human CD95 receptor intron 1 fragment.
                                                                                                                                                                                                                                                                                                                            11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                             AAZ88700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 ccaggcggagctgcctcttctcccgcgg 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
16-OCT-1998;
                               16-OCT-1998;
                                                              03-FEB-2000
                                                                                              DE19847779-C1.
                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 cgtccgcccacgcgtccgaccggggcttttcgtgagctcgtctctgatctcgcgcaagag 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccaggcggagctgcctcttctcccgcgg 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggctggagcctcaggggcgggcactggcacggaacacccctgaggccagccctggctgc 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggctggagcctcaggggcgggcactggcacggaacacccctgaggccagccctggctgc 1687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacgagtgactt 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                            (first entry)
98DE-1047779
                                 98DE-1047779
                                                                                                                                                                160..179
                                                                                                                                                                            Location/Qualifiers
                                                                                                                               /bound_moiety= p53
                                                                                                                                                 /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 190.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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WPI; 2000-628395/60
                                                                           12-APR-1999;
                                                (ISIS-) ISIS PHARM INC
                                                                                               10-APR-2000; 2000WO-US09540
                                                                                                                                                    WO200061150-A1.
                                                                                                                            19-OCT-2000.
                                                                                                                                                                                                                                                     Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis; Fas associated protein 1; protein tyrosine phosphatase; cancer; autoimmune disease; inflammatory disease; lymphoma; ss.
                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                          DNA encoding a human Fas (Apo-1) protein.
                                                                                                                                                                                                                                                                                                                                     06-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    AAC61798 standard; DNA; 2551 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1886 gcgggggcggggagagagcctgcagccttcagaacagatat 1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1766 aagctttagggtcgctggagggggaccccggttggagaggaggagcggaactcctggacaa 1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor intron 1 which contains a p53 binding region described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             226 gcggggggggggagagcctgcagccttcagaacagatat 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 aagotttagggtogctggagggggaccccggttggagagaggagcggaactcctggacaa 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 4; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-162245/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krammer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161;
                       Marcusson EG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mueller-Schilling M, Oren M;
                                                                       9905-0290640
                                                                                                                                                                           /product= "Fas"
                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 161; DB 21;
100.0%; Pred. No. 9.3e-35;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Barr PJ,
                     (LXRB-) LXR BIOTECHNOLOGY INC.
                                                 15-NOV-1993;
                                                                           15-NOV-1994;
                                                                                                     26-MAY-1995
                                                                                                                                                                                                                                    Key
                                                                                                                             W09513701-A
                                                                                                                                                                  mat_peptide
                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                          Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
adoptive immunotherapy; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                       Fas-delta-TM cDNA.
                                                                                                                                                                                                                                                                                                                                               06-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              AAQ93879 standard; cDNA; 2471 BP
                                                                                                                                                                                                                                                                                                                                                                             AAQ93879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1681 tggctgcccaggcggagctgcctcttctcccgcgg 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1621 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1561 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgaggggaagcggtttacga 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes human Fas (Apo-1). The specification describes antisense compounds which are targeted to the 5'-untranslated or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas plusphatase). The antisense compounds are used to inhibit the expression of Fas, FasL or Fap-1 in cells or tissues. They are used to treat autoimmune or inflammatory diseases such as hepatitis. They can also be used to treat cancer, especially colon, liver or lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 tggctgcccaggcggagctgcctcttctcccgcgg 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 71-73; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (Fap-1) expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB19341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.0%; Pues 155; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                               93US-0152443.
                                                                        94WO-US13173
                                                                                                                                                              /*tag= b
243..1136
                                                                                                                                                                                        195..242
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                                                                                                                                                     /*tag=
                                                                                                                                                                                                                             Location/Qualifiers
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100.0%; Pred. No. 1.8e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21; Length 2551;
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Kiefer MC,

Shapiro JP;

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AAX24878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA was obtd. from human lymphocytes and PCR was used to make cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCR product was ligated into pBluescript and the recombinant plasmid was used to transfect E. coli pH5-alpha cells insert sequence of pBluescript-Fas-delta-TM is given in AAQ93879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding Fas protein without its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Fas mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig.3-1 to 3-4; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAR76238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-200120/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1707 ctcccgcgg 1715
                                                                                                                                                                                                                                                                                          Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive; graft versus host disease; autoimmune disease; psoriasis; rheumatoid arthritis; systemic lupus erythematosus; gene therapy;
                                                                                                                                                                                                                                                                                                                                          Soluble Fas receptor DNA.
                                                                                                                                                                                                                                                                                                                                                                    21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   AAX24878 standard; DNA; 2471 BP.
                                                                                                                                                                                 sig_peptide
                                                                                                                                                                                                                                                           Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ctcccgcgg 129
                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 5.4%; Score 129; DB 16;
Local Similarity 100.0%; Pred. No. 3.2e-25;
nes 129; Conservative 0; Mismatches 0;
                        16-JUL-1998;
                                                                          W09903999-A1
                                                                                                          polyA_signal
                                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
   17-JUL-1997;
                                                28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggcactggcacggaacacaccctgaggccagccctggctgcccaggcgagctgcctctt 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggcactggcacggaacaccaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
  97US-0052829
                           98WO-US14771.
                                                                                                                                                            /*tag= b
243..1136
                                                                                                            /*tag= d
2455..2460
                                                                                                                                                                                   /transl_except= (pos:519..521, aa:Gly)
195..242
                                                                                                                                      /*tag= c
2349..2354
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lėngth 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
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AAQ29959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibition of proinflammatory responses - using an agent which modulates FasL stimulation, used for treating graft versus host disease or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This present sequence is a DNA clone encoding soluble Fas receptor (see AAW98070). The invention provides a method for inhibiting a proinflammatory response in a cell mixture by administering an immunosuppressive agent which inhibits the proinflammatory activity of Fas ligand (FasL). In some embodiments, FasL is coadministered with the immunosuppressive agent, and the cell mixture comprises with the immunosuppressive agent, and the cell mixture comprises.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 4B; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNMI ) UNIV MICHIGAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-132243/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1587 gacgcttctggggggtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1707 ctcccgcgg 1715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ29959 standard; cDNA to mRNA; 2534 BP
                                                                                                                                                                                                                                                                                                                                       12-MAR-1993 (first entry)
                                                                              sig_peptide
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                       Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss.
                                                                                                                                                                                                                                                                                       Human cell surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watch 5.4%; Score 129; DB 20;
Local Similarity 100.0%; Pred. No. 3.2e-25;
nes 129; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 1706
                                 /*tag= a
243..1199
                                                                                    Location/Qualifiers
195..242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The method can be practised in vitro, ex vivo or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20; Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Gaps

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mat\_peptide

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AAQ95297
                                                                                                                     RESULT 10
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                           19-FEB-1996 (first entry)
                                                                                 AAQ95297 standard; cDNA; 2534 BP
                                                                                                                                                                         1707 ctcccgcgg 1715
                                                             AAQ95297;
                                                                                                                                                                                                                                                                                                                                                                                                                           A cDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The CDNA was ligated to BstXI-cut vector pCEV4 via BstXI linkers. The KT3 cDNA library was used to transfect monkey COS-Ab. The cells were then suspended in buffer containing murine anti-Fas antibodies. The Fas-expressing cells adhered to the plates. Extrachromosomal DNA was prepared from adhered to the plates. transform E.coli VM100 cells. A 520bp XhoI-BamHI fragment from a longest cDNA clone was designated pF58 and contains an ORF corresp. to a 335 amino acid pre-protein and a 319 amino acid mature protein
                                                                                                                                                                                                                                                 1647
                                                                                                                                                                                                                                                                           1587 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 1646
                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 1 and 2; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monoclonal antibodies that react with tumour cells expressing Fas
                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR28084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-358914/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (OSAB-) OSAKA BIOSCIENCE INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP510691-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-OCT-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyA_signal
                                                                                                                                                                                                                                                            1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conflict
                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                      99cactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                          ctcccgcgg 129
                                                                                                                                                                                                                     99cact99cac9gaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 1706
                                                                                                                                                                                                                                                                                                                                 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagata s,
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91JP-0125234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92EP-0107060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= d
2352..2357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "this residue is not present in pF3"
1831..1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= Fas_antigen 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                      5.4%; Score 129; DB 13; 100.0%; Pred. No. 3.3e-25; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..2523
f
                                                                                                                                                                                                                                                                                                                                                 Length 2534;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                     AAT16303
                                                                                                                                                                                  RESULT 11
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                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Synthetic.
             Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE; rheumatoid arthritis; serum; systemic lupus erythematosus; ss.
                                                            hFas coding sequence from plasmid pCEV4/hFas.
                                                                                             06-SEP-1996 (first entry)
                                                                                                                            AAT16303;
                                                                                                                                                   AAT16303 standard; cDNA; 2534 BP
                                                                                                                                                                                                                                        1707 ctcccgcgg 1715
                                                                                                                                                                                                                                                                                    1647 ggcactggcacggaacacccctgaggccagccctggctgcccaggcggagctgcctctt 1706
                                                                                                                                                                                                                                                                                                                                          1587 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ95297 is the plasmid pr58 which contains the human Fas cDNA. The plasmid was used in the construction of an expression vector for the prodn. of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of related diseases.
                                                                                                                                                                                                                         121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Pages 15-17; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR78606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1993;
                                                                                                                                                                                                                                                                     61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP07115988-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody production; diseases; treatment; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pF58; human Fas cDNA; soluble membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pF58 contg. human Fas cDNA.
                                                                                                                                                                                                                                                                                                                           1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1995-202847/27.
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93JP-0267644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93JP-0267644.
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243..1199
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195..2
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                                                                                                                                                                                                                                                                                                                                                                                     5.4%; Score 129; DB 16;
100.0%; Pred. No. 3.3e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..242
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9601277-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the coding sequence for the human Fas antigen contained within the plasmid pCEV4/hFas. The soluble Fas antigen is included in the immunoassay kit of the invention. The kit is for the assay of soluble Fas antigen and contains an immobilised anti-soluble Fas antigen encoded monoclonal antibody, as well as the standard soluble Fas antigen encoded by this sequence. The assay is simple and has high accuracy, high by this sequence of assaying a number of different specimens sensitivity, and is capable of assaying a number of different specimens at the same time. The immunoassay is used on biological samples (such as serum) and is useful for diagnosis of autoimmune diseases such as rheumatoid arthritis or systemic lupus erythematosus (SIE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD. (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoassay method for soluble Fas antigen in body fluids - for diagnosis of auto:immune diseases such as rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hachiya T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Page 49-52; 124pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       systemic lupus erythematosus
                                                                                                                                                                                                                                 1647 ggcactggcacggaacacacctgaggccagccctggctgcccaggcggagctgcctctt 1706
                                                                                                                                                                                                                                                                                            1587 gacgcttctggggggtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 1646
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2534 BP; 817 A; 488 C; 502 G; 727 T; 0 other;
                                                                                                     2993
                                                                                     AAV32993 standard; cDNA; 2534 BP
Fas cDNA
                            18-NOV-1998
                                                        AAV32993;
                                                                                                                                                            121 ctcccgcgg 129
                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                              1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1996-087635/09.
                                                                                                                                                                             ctcccgcgg 1715
                                                                                                                                                                                                                    ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Noguchi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95JP-0025637.
94JP-0154706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-JP00349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
243..1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= Fas antigen
195..242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yonehara S;
                                                                                                                                                                                                                                                                                                                                                                                 DB 17; Length 2534;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                           Gaps
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Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL; CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV; simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                           Mammalia sp.
                                                                                                                                                                                                                                                                                                                                                                                                        prophylactic; AIDS; ss.
                                                                                                                                                                                                                                                                                                                        polyA_signal
                                                                                                                                                                                                                                                                                                     W09835692-A1
                                                                                                                                                                                                                                                (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                              17-FEB-1997;
                                                                                                                                                                                                                                                                           17-FEB-1998;
                                                                                                                                                                                                                                                                                        20-AUG-1998.
                                                                                                                                                                                                                       WPI; 1998-456867/39.
                                                                                                                                                                                                                                    Screaton GR,
                                                                                                                                                                                                                P-PSDB; AAW49104.
                                                                                                                                                                                                                                      Xu X;
                                                                                                                                                                                                                                                                97GB-0003276
                                                                                                                                                                                                                                                                             98WO-GB00485
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195..242
/*tag= b
243..1199
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1831..1836
                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                             "Fas protein"
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Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency diseases - by interfering with interaction of Fas with Fas-ligand expressed on activated CD4+ cells, e.g. cells infected with HIV

Disclosure; Fig 10; 71pp; English.

The present sequence represents a Fas cDNA sequence used in the CC method of the invention. The method is concerned with reducing CC method of the invention. The method is concerned with reducing CC depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK) CC (Fast)-expressing activated CD4+ cells. It involves contacting this CC (Fast)-expressing activated CD4+ cells. It involves contacting this CC immune cell population with an effective amount of an agent (e.g. a CC immune cell population which would interfere with the CC interaction between Fas and Fast. Therefore, the method is useful for CC interaction between Fas and Fast. Therefore, the method is useful for CC interaction between Fas and Fast. The populations of activated CC identifying suitable agents which can reduce depletion of activated CC identifying suitable agents which can reduce depletions of the Signature of the manufacture of therapeutic compositions. CC is the use of the Signature of the manufacture of therapeutic compositions. CC is the use of the Signature of the manufacture of therapeutic compositions. CC cell surface receptor Fas and its ligand Fast. By interfering with CC expoptosis of CD8+ TK lymphocytes caused by expression of Fast on CC apoptosis of CD8+ TK lymphocytes caused by expression of Fast on CC apoptosis of CD8+ TK lymphocytes caused by expression of Fast on CC activated CD4+ cells. Such Fast-expressing activated CD4+ cells are activated CD4+ cells. The method described with the infection with an immunodeficiency virus (SIV). The claimed prevention of apoptosis may then allow virus (SIV). The claimed prevention of apoptosis may then allow the composition of cytotoxic Tlymphocyte (CTL) activity constraint (prophylactic and/or therapeutic) of immunodeficiency creatment (prophylactic and/or therapeutic) of immunodeficiency creatm diseases e.g. AIDS.

Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

δõ Matches 129; Query Match Local Similarity Conservative 100.0%; 5.4%; Score 129; DB 19; 100.0%; Pred. No. 3.3e-25; 0; Mismatches DB 19; Length 2534; Indels 0; Gaps

В

Query Match

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AAV07002
                         The present sequence was used in the development of novel Fas antigen derivatives, which contain a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the 1st cysteine residue. The derivatives are effective regulators of apoptosis and can be of the coding DNA in gene therapy) to treat a range of diseases, such as hepatitis, influenza and HIV, by modulating apoptosis of such as hepatitis, influenza and HIV, by modulating apoptosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Дb
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Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;
                                                                                                                                                                     Disclosure; Fig 1-2; 102pp; Japanese.
                                                                                                                                                                                        has low antigenicity, promotes apoptosis and is useful in treatment of viral and other diseases
                                                                                                                                                                                                              Fas antigen derivative containing modified extracellular region
                                                                                                                                                                                                                                                    P-PSDB; AAW50289
                                                                                                                                                                                                                                                             WPI; 1997-558981/51.
                                                                                                                                                                                                                                                                                    Nagata S, Nakamura N;
                                                                                                                                                                                                                                                                                                                                               02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-1997
                                                                                                                                                                                                                                                                                                        (MOCH ) MOCHIDA PHARM CO LTD.
(OSAB-) OSAKA BIOSCIENCE INST
                                                                                                                                                                                                                                                                                                                                                                                                                    W09742319-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Fas antigen cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV07002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1647 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 60
                                                                                                                                                                                                                                                                                                                                           96JP-0135760.
                                                                                                                                                                                                                                                                                                                                                                  97WO-JP01502.
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195..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= Fas_antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                               Shuttle vector pAdDel.CMVDys (AAT27558) comprises the adenovirus cis elements needed for replication and virion encapsidation but is deleted of all viral genes. It carries a mouse dystrophin virus that supplies the sequences needed for a productive viral infection but which has disabled packaging function. Recombinant delivery to host cells and the ability to stably integrate the to transfer the dystrophin gene for use in muscular dystrophy gene therapy.
Sequence 19307 BP; 4816 A; 4393 C; 4056 G; 6042 T; 0 other:
                                                                                                                                                                                               Example 9; Fig 12A-12P; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.28; Matches 128; Conservative
                                                                                                                                                                                                                              transgene(s) to target cells
                                                                                                                                                                                                                                 Recombinant adenovirus produced from shuttle vector and helper virus has crippled packaging function, useful for delivering
                                                                                                                                                                                                                                                                                      WPI; 1996-251463/25.
                                                                                                                                                                                                                                                                                                         Chen S, Fisher KJ, Weitzman M, Wilson JM;
                                                                                                                                                                                                                                                                                                                                          (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                       28-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                  27-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adenovirus type 5; Ad5; vector; gene therapy; gene transfer; helper virus; dystrophin; muscular dystrophy; ds; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9613597-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shuttle vector pAdDel.CMVDys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1647 ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 1706
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                                                                                                                                                                                                                                                                                                                                                                                              95WO-US14017
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Pred. No. 9.2e-25;
0; Mismatches 1;
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Matches Query Match Best Local 9

93;

Conservative

0;

Mismatches

49;

Indels

0; Gaps

Local Similarity

2.78;

Score 63.6; DB 17; Length 19307; Pred. No. 2.2e-06;

1667 cctgaggccagccctggctgcccaggcggagctgcctcttctcccgcggacatgtacaga 1726

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RESULT 15
AAT27557/c
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16048 ccggccgcctgcagctggcgccatcgatacgcgtacgtcgcgaccgcggacatgtacaga 16107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adenovirus type 5; Ad5; vector; gene therapy; gene transfer; helper virus; cystic fibrosis transmembrane conductance regulator; CFTR; ds; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT27557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT27557 standard; cDNA; 9972 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shuttle vector pAdDel.CBCFTRZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                     WO9613597-A2
 WPI; 1996-251463/25
                     Chen S,
                                                            28-OCT-1994;
                                                                               27-OCT-1995;
                                       (UYPE-) UNIV PENNSYLVANIA.
                     Fisher KJ, Weitzman M,
                                                            94US-0331381.
                                                                               95WO-US14017.
                                                                                                                                                                                                                                                                                                                                                                                                /note= "3' adenovirus inverted terminal repeat" complement (3887..3684)
                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (3652..3073)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                   /function= packaging sequence PAC I complement (9353..9340)
                                                                                                                                                                                                                                                                               /note= "5' adenovirus inverted terminal repeat" complement (9374..9360)
                                                                                                                                                                                                                                                                                                                                                                               complement (8622..4065)
                                                                                                                                                                                                                                                                                          /rpt_type= INVERTED
/note= "5' adenoviru
                                                                                                                                                                                                                     /function= packaging sequence PAC complement (9311. 9298)
                                                                                                                                                                                                                                                                                                                     /function= CMV enhancer/beta actin promoter complement (9611..9254)
                                                                                                                                                                                                                                                                                                                                                    /function= CFTR gene
complement (9241..8684)
                                                                                                                                                           /function= packaging sequence PAC IV complement (9276..9263)
                                                                                                                                                                                       /function= packaging sequence PAC III complement (9301..9288)
                                                                                                                                        /function= packaging sequence PAC V
                                                                                                                                                                                                                                                                                                                                                                                                                       INVERTED
                        Wilson JM;
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant adenovirus produced from shuttle vector and helper virus - has crippled packaging function, useful for delivering transgene(s) to target cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Fig 7A-7H; 149pp; English.
                                                                                                                                                                                                     1668 ctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgggacatgtacagag 1727
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9972 BP; 2581 A; 2362 C; 2245 G; 2784 T; 0 other;
                                                                                                                                                                             2980 CGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGAG 2921
                                                                                      2920 CTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTGGCACTGGCCGTCGTT 2861
                                                                                                              1728 ctcgagaagtactagtgggccacgtggggcgcgtgcaccttaagctttagggtcgctggaggg 1787
2860 TTACAACGTCGTGACTGGGAA 2840
                                        1788 ggaccccggttggagagagga 1808
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Pred. No. 2.9e-06;
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search completed: September
Job time: 30007 sec 7, 2002, 18:41:53 B

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                              Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/
2: /cgn2_6/ptodata/2/
3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
5: /cgn2_6/ptodata/2/
6: /cgn2_6/ptodata/2/
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Match Length DB
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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US-08-232-463-14
US-08-232-463-14
US-08-232-63-10
US-08-232-63-10
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US-08-332-766A-8

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US-09-417-455-7

US-09-418-584A-9

US-09-018-584A-9

US-08-713-557B-35

US-08-458-434A-6

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US-08-483-553-24

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ALIGNMENTS	US-08-483-554B-24 US-08-880-727-24 PCT-US95-10202-24 PCT-US95-10202-24 PCT-US95-10202-24 PCT-US95-1020-24 US-08-332-766A-27 US-08-332-766A-21 US-09-488-671-10 US-09-488-671-10 US-09-78-294-3 US-08-332-766A-10 US-09-018-84A-19 US-08-623-906A-13
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US-09-290-640-1
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DATABASE ENTRY DATE: 1996-07-19
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LOCATION: (221)...(1228)
PUBLICATION : TOORNATION:
JOURNAL: J. Biol. Chem.
VOLUME: 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09290640 Patent No. 6204055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 2551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling FILE REPERENCE: ISH-0351
                                                                                                                                                                                                                                   Ouery Match 6.5%; Score 155; DB 4; Length 2551; Best Local Similarity 100.0%; Pred. No. 1.5e-32; Matches 155; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dean, Nicholas M. APPLICANT: Marcusson, Eric G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  ISSUE: 15
PAGES: 10709-10715
DATE: 1992-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                            1561 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgaggggaagcggtttacga 1620
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tggctgcccaggcggagctgcctcttctcccgcgg 155
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               Sequence 18, Application US/08152443A Patent No. 5663070
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 18:
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LOCATION: 195.
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          61 GCACTGGCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0:
FILING DATE: 15-NOV-1993
ATTORNEY_AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                      1 GACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCG 60
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: LEHNHARDT, SUSAN K. REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/OFFILING DATE: 18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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SHAPIRO,
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VENTION: NOVEL FAS PROTEIN AND METHODS OF USE
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US-08-219-237B-1
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; LOCATION: 243
US-08-152-443A-18
                                                                                                    Sequence 1, Application US/08219237B Patent No. 5874546
                                                                                                                                                                                                                                                                                                                                                                                Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                        GENERAL INFORMATION:
   APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 18:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                             .121 CTCCCGCGG 129
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 813-5600 TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                      1 GACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCG 60
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STATE: California
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195..1136
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SHAPIRO, JOHN P.
KIEFER, MICHAEL C.
VENTION: NOVEL FAS PROTEIN AND METHODS OF USE
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No. 1.9e-25;
ative 0; Mismatches 0;
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ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 5167
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
                                                                                                                             US-08-219-237B-1
                                        Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
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MEDIUM TYPE: Floppy
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APPLICATION NUMBER: US 07/872,129
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LIBRARY: pCEV4
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ORIGINAL SOURCE:
1587 gacgottotggggagtgagggaagcggtttacgagtgacttgg\dot{
m p}ctggagcotcaggggcg 1646
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide LOCATION: 243..1199
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                                                                                                                                              NAME/KEY: polyA_site LOCATION: 2518..2523 IDENTIFICATION METHOD: IDENTIFICATION METHOD:
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LOCATION: 2352..2357
IDENTIFICATION METHOD:
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195..1202
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                                        5.4%; Score 129; DB 2; Length 2534 illarity 100.0%; Pred. No. 2e-25; Conservative 0; Mismatches 0; Indels
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1831..1836
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                                                                                    Length 2534;
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||||||||
121 cTCCCGCGG 129
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TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1647 ggcactggcacggaacacccctgaggccagccctggctgcccaggcggagctgcctctt 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE TITLE OF INVENTION: ANTIGEN NUMBER OF SEQUENCES: 11
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MURPHY JK., JAMES 128,977
REGISTRATION NUMBER: 28,977
REFERENCE_DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGCACTGGCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTT 120
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/468,560C FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                               LENGTH: 2534 base pairs TYPE: nucleic acid STRANDEDNESS: double
NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                     NAME/KEY:
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P.O. BOX 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                  linear
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195..242
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                                            polyA_site
2352..2357
                                                                                                                                                                                                                            195..1202
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 polyA_site
2518..2532
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                                                                                         polyA_site
1831..1836
                                                                                                                                                                                                                                                                                                  cDNA to mRNA
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US-08-468-560C-1

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APPLICANT: NAKAHURA, NO. 630639510

APPLICANT: NAKAHURA, NO. 630639510

TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE

FILE REFERENCE: 1110-207p

CURRENT APPLICATION NUMBER: US/09/180,100

CURRENT FILING DATE: 1998-11-02

EARLIER APPLICATION UNMBER: PCT/JP97/01502

EARLIER FILING DATE: 1997-05-01

NUMBER OF SEQ ID NOS: 25

SOFTMARE: Patentin Ver. 2.0

LENGTH: 2534
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; ORGANISM: Homo sapiens
US-09-180-100-16
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Sequence 16, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
                                                                                                                                                                                      Patent No. 5670367
GENERAL INFORMATION:
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                                                                                                                                                                                                              Sequence 14, Application US/08232463 Patent No. 5670367
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                                                   APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               1707 ctcccgcgg 1715
                                                                                                                                                                                                                                                                                                                                                                                                                           1647 ggcactggcacggaacacacctgaggccagccctggctgcccaggcggagctgcctctt 1706
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STREET: 1800 Dia
CITY: Alexandria
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                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GCACTGGCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
      E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.4%; Score 129; DB 4; Length 2534; 100.0%; Pred. No. 2e-25; rative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
1432 YYYGTACCAAATTCT 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 91
ETLING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                  363 tgtctattagatgct 377
                                                                                                                               303 atttgcagagataatacagagaatgcccatataccatcctccttatcccacttctttttg 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 tittacattitittatttaaatgaactiitcattitggaatagtiitaggatticaaaaa 302
                                                                                                                                                                                                                                                                                                                                   183 ttccattccttccttaccttacctctcctttccttccctcacaccccttttccttccttct 242
                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 ctataatgataagtattaagtaaggaagatccacatatgtgagttgctggcttataattc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 cttttttggctacatttttttatttgtaaagtaagtttaataatcactcatctcactggg 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 3.0%; Score 71.8; DB 1; Length 7218; Similarity 1.9%; Pred. No. 1.5e-09; 7; Conservative 238; Mismatches 130; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22313-0299
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US-08-232-463-14/c ; Sequence 14, Application US/08232463 ; Patent No. 5670367

RESULT

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CLONE: pTZgpt-F1s
US-08-232-463-14
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 14:
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ZIP: 22313-0427
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Fl
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria
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480 ggtggtaagtgcagtgacagatgcaaaacacagggtgatggaaagccctcaggagggtaa 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420 tggcactaacagtctactgaaaggtggaacagagacaagcctatcaacacctacaagact 479
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APPLICATION NUMBER:
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                                                       660 taattgggaagggagagagttgcagagtgaggtgcagagcttggtggacgatgccaaag 719
                                                                                                                                                                                          600 ctgaaggatgaacagtgggctaagcaaagggttattaatgtgttattaatgggttgaatc 659
                                                                                                                                                                                                                                                                                                                       540 cctaacctagatttgagggcccaaacaggctccagaagaaaatgtcaactgagaggaagc 599
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899149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.8%; Score 67.4; DB 1;
ilarity 8.0%; Pred. No. 2.5e-08;
Conservative 228; Mismatches 174;
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US-08-836-022A-10
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; Patent No. 6001557
                                                                                                                                                                                                                                                                                              US-08-836-022A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                       Query Match 2.7%; Score 63.6; DB 3; Length 19307; Best Local Similarity 65.5%; Pred. No. 4.6e-07; Matches 93; Conservative 0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1022 GTGAGCGTATGGCAAAC 1006
                                                                                                                                       16048 CCGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGA 16107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chen, Shu-Jen
APPLICANT: Weitzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
16168 TTTACAACGTCGTGACTGGGAA 16189
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,381
FILING DATE: 28-OCT-1994
                                                                                                                                                                                                                                                                                                                TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    1667 cctgaggccagccctggctgcccaggcggagctgcctcttctcccgcggacatgtacaga 1726
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                               1787 gggaccccggttggagagagga 1808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: Z15 TELEPHONE: Z15-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bak, Mary E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                    19307 base pairs
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                                                                                                                                                                                                                                                                                                                               unknown
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RESULT 11
US-08-836-022A-3/c
; Sequence 3, Application US/08836022A
; Patent No. 6001557
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APPLICATION NUMBER: 08/836,022
FILLING DATE: CUNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVPN.008PCT
TELEPHONE: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-427-048A-10
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                                                                                                                                                                                        16108 GCTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTGGCACTGGCCGTCGT 16167
                                                                                                                                                                                                                                                                       16048 CCGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGA 16107
                                                                                                                     16168 TTTACAACGTCGTGACTGGGAA 16189
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                             1667 cetgaggeeageeetggetgeeetaggeggagetgeetetteteeegeggaeatgtaeaga 1726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown MOLECULE TYPE: CDNA
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FILING DATE: 21-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weitzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                         2.7%; Score 63.6; DB 4; Length 19307; 11 Similarity 65.5%; Pred. No. 4.6e-07; 93; Conservative 0; Mismarchco
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COUNTRY: USA
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Fisher, Krishna J.
Chen, Shu-Jen
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US-09-427-048A-3/c
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                                                                                                                           Sequence 3, Application US/09427048A Patent No. 6203975
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 215-540-5040
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9972 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                       2980 CGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGAG 2921
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REFERENCE/DOCKET NUMBER: GNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
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FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,022A
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Trustee, James M.
APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
Chu-Jen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
            TITLE OF INVENTION: Improved Adenovirus Virus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                  APPLICANT: Trustees of the University of Pennsylvania
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                                                          Chen, Shu-Jen
                                                                        Fisher, Krishna J.
                                  Weitzman, Matthew
                                                                                      Wilson, James M.
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Methods of Use Thereof
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US-09-427-048A-3
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SEQUENCE CHARACTERISTICS:
LENGTH: 9972 base pairs
                                                                                                                                                                                              APPLICANT: Camero APPLICANT: Shaw,
                                                                                                                      APPLICANT: Cameron, Douglas C. APPLICANT: Shaw, Anita J. APPLICANT: APPLICANT: ANITAGE STATE OF INVENTION: MICROBIAL PROTITLE OF INVENTION: FROM SUGAR NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                      1668 ctgaggccagccotggctgcccaggcggagctgcctcttctcccgcgggacatgtacagag 1727
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                                                                                                       CORRESPONDENCE ADDRESS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,022
FILING DATE: <Unknown>
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NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: GNVPN.008PCT TELECOMMUNICATION INFORMATION:
               COUNTRY:
                                   STATE: WI
                                                                      STREET:
                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92; Conservative
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STRANDEDNESS: double
RY: U.S.A.
53717-1914
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                                                      Madison
                                                                      E: DeWitt Ross & Stevens S.C.
8000 Excelsior Drive, Suite 401
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                                                                                                                                                               MICROBIAL PRODUCTION OF 1,2 PROPANEDIOL
                                                                                                                                                 FROM SUGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Pred. No. 6e-07;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4476 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGIA
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1668 ctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgggacatgtacagag 1727
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cameron, Dou
APPLICANT: Shaw, Anita
APPLICANT: Altaras, Ned
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/498,599
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MICROSIAL PRODUCTION OF TITLE OF INVENTION: 1,2-PROPANEDIOL FROM SUGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          523 CGGCCGCCTGCAGCTGGCGCCATCGATACGCGTACGTCGCGACCGCGGACATGTACAGAG 582
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
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             ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER:
REFERENCE/DOCKET NECEMBART
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whatch 2.6%; Score 62.4; DB 3; Length 4476; Local Similarity 75.0%; Pred. No. 4.4e-07; Pres. 78; Conservative 0; Mismatches 26; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                 CITY: Madison
                                                                                                                                                                                                                                                                                                                   STREET:
                                                                         CLASSIFICATION:
                                                                                           FILING DATE:
                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                 ΣH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                   E: DeWitt Ross & Stevens S.C.
8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cameron, Douglas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vector pSE380
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TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

TELEPHONE:

: 608-831-2100 608-831-2106

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US-08-306-691B-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/08306691B Patent No. 5734039
                                                                                                            TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US
FILING DATE: September
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Best Local S
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                             SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                             NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SKOTSKI, TOMASZ
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
ADDRESSE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1728 ctcgagaagtactagtggccacgtgggccgtgcaccttaagctt 1771
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                                                                                                                                   TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DN
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 2.6%; Score 62.4; DB 4; Length 4476; Local Similarity 75.0%; Pred. No. 4.4e-07; nes 78; Conservative 0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calabretta, Bruno
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                                                                                                                                                                                                                                                                                                                                                   September 15, 1994
N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette, 3.50 inch, 720 kb
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                                                                                                                                                                                             Best Local Similarity 55.6 Matches 115; Conservative
                                                                                                                                                                                                             Query Match
Best Local :
3986 TTCTTTCTTTTTCTATCTTTTGAGA 4012
                                        3806 GAGGTTGCAGTGAGCTGAGATCATGCCACTGCACTCCAGCCTAGGCGACAGAGCAAGACT 3865
              267 acttttcattttggaatagttttagga 293
                                                                                                     87 gaagatocacatatgtgagttgotggottataattcacactcaagagatactgattttgt 146
                                                                                                                                                                                     2.5%; Score 59.8; DB 1; Length 35100; 55.6%; Pred. No. 6.9e-06; Vative 0; Mismatches 92; Indels 0;
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Search completed: September 7, 2002, 18:26:08 Job time: 29062 sec

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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1 agctttttttggctacatttt.....tggctaatcaaagagacgtg 2380
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                                             cgn2_6/ptodata/2/pna/US07_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

27 27 28 29 20 21 21 21 21 22 23 23 23 24 25 26 27 27 28	Result No.
1923 1899 1711 1711 1377 1377 1377 1377 1377 13	Score
100.0 90.8 72.0 72.0 72.0 72.7 57.7 57.7 17.8 117.8 117.8 110.1 110	Query Match
4. Ω ΕΙ Μ Μ Μ ΙΙ Ν Ν	Match Length
362 362 362 363 363 363 363 363 363 363	DB 32
US-09-834-291-4 US-09-937-722-10 US-09-834-291-1 US-09-82-665-615B-94 US-08-377-522-1 US-08-377-522-1 US-08-377-522-1 US-08-377-522-1 US-08-377-522-1 US-08-377-522-1 US-09-34-291-674 US-09-934-291-674 US-09-934-291-674 US-09-952-4-038-674 US-09-952-816-3367 US-09-952-816-3367 US-09-726-172-360-3705 US-09-726-172-3031 US-09-726-172-3031 US-09-726-172-3031 US-09-726-172-3031 US-09-726-172-3031 US-09-726-172-3031 US-09-726-172-3031 US-09-726-172-3031 US-09-726-172-3031 US-09-726-810-2456 US-09-726-810-2456 US-09-760-445-327 US-60-172-373-15844 US-60-172-373-15844 US-60-173-360-1236 US-09-287-618-11167 PCT-US00-05883-187 US-09-726-983-187 US-09-726-983-187	-291-
111322498837	Description Sequence 3, Appli

App App App App App D 541 ctaacctagatttgagggcccaaacaggctccagaagaanaatgtcaactgagagg App App D 541 ctaacctagatttgagggcccaaacaggctccagaagaacatgtcaactgagagg App App D 541 ctaacctagatttgagggcccaaacaggctccagaagaacttaattggttag D 661 aattgggaaagggaagggttagaaggttaaaggagttaattaatggttag D 661 aattgggaaagggaagggttagaaggttagaaggttaattaatggttag D 721 aatactgaaaccttagtggttagaaggttagaaggttaattaa	166.4 7.0 263 12 US-08-835-540 Sequence 166.4 7.0 263 40 US-08-931-581 Sequence 166.4 7.0 263 20 US-09-834 291-581 Sequence 26 201-31-31 Sequence 27 Sequence 28 Application US/09834291  ALIGNMENTS  1
2214, Ap  2214, Ap  2214, Ap  2318, Ap  2645, Ap  3879, Ap  39624, A  310, Ap  481 gtggtaagtgcagtgacaggtggacaagcctatcaacagctctaccagagact	32 190.2 8.0 466 17 US-09-333-909-2214 33 190.2 8.0 466 31 US-09-817-500-2214 Sequence 34 188.4 7.9 532 29 US-09-72645 35 188 7.9 565 25 US-09-652-124-2645 Sequence 36 182.6 7.7 473 16 US-09-248-1797-39624 Sequence 37 182.6 7.7 473 16 US-09-248-1797-39624 Sequence 38 182.6 7.7 473 16 US-09-248-1797-39624 Sequence 39 182.6 7.7 473 34 US-09-948-9973-96624 40 179.6 7.5 453 29 US-09-726-788-4710 Sequence 41 178.8 7.5 462 28 US-09-726-788-4710 Sequence 42 178.8 7.5 462 28 US-09-726-788-4710 Sequence

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                                                                                                                                         US-09-834-291-4
                                                                                                       Sequence 4, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter AppLICANT: Muller-Schilling, Martina AppLICANT: Oren, Moshe TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122 CURRENT APPLICATION (UMBER: US/09/834,291 CURRENT FILING DATE: 2001-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1501 aggetteetteecateeteetgaceaeeggggettttegtgagetegtetetgateteege 1560 | 1501 aggetteetteeteeteetgaceaeeggggettttegtgagetegtetetgateteege 1560 | 1501 aggetteetteeteeteetgaceaeeggggettttegtgagetegteetgatetege 1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agagaggagcggaactcctggacaagccctgacaagccaaagccaaaggtccgctccggcg
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PRIOR EILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
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                                    2308 cgggtgggtgagtgcgccgccgccgcgggggggggggagagagcctgcagccttcagaac
                                                       1861 cgggtgggtgagtgcgccgcccgcgggggggggggggagagagcctgcagccttcagaac 1920
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GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
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CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
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APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                   8501 ggctataatgataagtattaagtaaggaagatccacatatgtgagttgctggcttataat 8560
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                    2788 cagaaatgccagcttgcagatggctaatcaaagagacgtg
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; TYPE: DNA
; ORGANISM: Homo Sapiens
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PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
                                       11201 tcaaagagacgtg 11213
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84.9%;
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Pred. No. 0;
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APPLICANT: Wyatt, Jacqueline
TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0502
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US-09-802-669-94
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APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
NUMBER OF SEQ ID NOS: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 94, Application US/09802669 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marcusson, Eric G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dean, Nicholas M.
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2165
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                  1682 tggctgcccaggcggagctgcctcttctcccgcgg 1716
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                                                                                                                                                                                                                                                                                         Y Match 72.0%; Score 1713.4; Local Similarity 99.9%; Pred. No. 0;
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GENERAL INFORMATION:
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                                                                                                       INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                        SEQUENCE CHARACTERISTICS:
            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
CITY: I
STATE:
FEATURE:
                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                    TELEPHONE:
                                             STRANDEDNESS: single
                                TOPOLOGY:
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                                                          nucleic acid
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                                                                             1608 base pairs
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Koopman, William
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512/474-7577
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; NAME/KEY: ; LOCATION: US-08-377-522-1

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Best Local Similarity
1160 aaatgccccgcaagtctttctctgagtgactccagcaattagccaaggctcctgtaccca 1219
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                                                847 AAATGCCCCGCAAGTCTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCA
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                                                                                                                                                                                         GGCTATGCGATTTGGCTTAAGTTGTTAGCTTTGTTTTCCTCTTGAGAAATAAAAACTAAG
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99.4%;
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; GENERAL INFORMATION:
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                                                                                           TELEFAX: (713) 777-69
INFORMATION FOR SEQ ID NO:
              MOLECULE TYPE:
                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1608 bp
                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.,
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919
                                                                                                                                                                                                                           APPLICATION NUMBER: UFILING DATE: January CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               STATE: TX
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Human Fas Gene Promoter Region NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1700 gcctcttctcccgcgg 1715
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STRANDEDNESS: doub
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                      linear
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genomic DNA
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IMMEDIATE SOURCE:
LIBRARY: (FIXII; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMB-
POSITION IN GENOME:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08377522D GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
                                                                       FILING DATE: January CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                      CURRENT APPLICATION DATA:
NAME: Benjamin Aaron Adler, Ph.D., REGISTRATION NUMBER: 35,423
REGISTRATION NUMBER: D5919
                                                                                                                                                                                                                  STREET:
CITY: F
STATE:
                                                                                                                                             COMPUTER: Apple Macintosh OPERATING SYSTEM: Macinto
                                                                                                                                    SOFTWARE:
                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                          ADDRESSEE:
                                                 FILING DATE:
                                                           APPLICATION NUMBER:
                                                                                                          APPLICATION NUMBER: US/08/377,522D
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                                                                                                                                                                                                                                Houston
                                                                                                                                                                                                                                            E: Benjamin Aaron Adler,
8011 Candle Lane
                                                                                                                                                                                                                                                                                                      Mountz et al.
                                                                                                                                    Microsoft Word for Macintosh
                                                                                                January 20, 1995
                                                                                                                                                                                                                                                                                            Human Fas Gene Promoter Region
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DESCRIPTION: G
HYPOTHETICAL: nc
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TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                  487
                                                                                                                                                                   427
                                                                                                                                                                                                                                                           680 ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg 739
                                                                                                                                                                                             740
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LIBRARY: (FIXII; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMB
                                                                                                                                                                                                                                                                                                               247 CCAAACAGGCTCCAGAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: doub.
TOPOLOGY: linear
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CCTTCTGTAAAATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTG
                                                                                                                    ccttctgtaaaattcatgctaaactacctaagagctatctaccgttccaaagcaatagtg
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CURRENT APPLICATION NUMBER: US/60/324,185 CURRENT FILING DATE: 2001-09-21 NUMBER OF SEQ ID NOS: 35862 SOFTWARE: PERL Program SEQ ID NO 29531 LENGTH: 3814 TYPE: DNA

ORGANISM: Homo sapiens

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US-60-324-185-29531
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Sequence 29531, Application US/60324185
GENERAL INFORMATION:
APPLICANT: MORTALS, MacDonald
APPLICANT: MORTALS, MacDonald
APPLICANT: Lale, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
FILE REFERENCE: GX-0019-1 p
FILE REFERENCE: GX-0019-1 p
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                                                                                             RESULT 11
US-09-834-291-2
; Sequence 2, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; APPLICANT: Oren, Moshe
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OTHER INFORMATION: Incyte ID No: 415714.1
TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122 CURRENT APPLICATION NUMBER: US/09/834,291 CURRENT FILING DATE: 2001-08-21 PRIOR APPLICATION NUMBER: PCT/DE99/03343 PRIOR FILING DATE: 1999-10-18 PRIOR APPLICATION NUMBER: DE 198 47 779.1
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Pred. No. 2e-141;
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Sequence 674, Application (Seneral INCORATION)
GENERAL INCORATION:
APPLICANT: Hyseq, In:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 2041
CUBRENT STITIG DATE:
CUBRENT STITIG DATE:

APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 20411-780
CURRENT APPLICATION NUMBER: US/09/404,284
CURRENT FILING DATE: 1999-09-21
CURRENT FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 4670
NUMBER OF SEQ ID NOS: 4670

SOFTWARE: Hy-patent.pl Version 3.1 SEQ ID NO 674

LENGTH: 449

US-09-404-284-674/c

Sequence 674, Application US/09404284

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; TYPE: DNA; ORGANISM: Homo Sapiens US-09-834-291-2
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SEQ ID NO 2
LENGTH: 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1766 aagetttagggtegettggagggggaceceggttggagaggagggggaacteetggacaa 1825
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                 aatcaaagagacgtg 2380
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aatcaaagagacgtg 720
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99.7%;
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Sequence 674, Application US/09524038
GENERAL IMFORMATION:
APPLICANT: Dimenac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark C.
APPLICANT: Ones, Lee w.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obt
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 780CIP
CURRENT APPLICATION NUMBER: US/09/524,038
CURRENT FILING DATE: 2000-03-13
EARLIER APPLICATION NUMBER: 09/404,284
EARLIER FILING DATE: 1999-09-21
NUMBER OF SEO ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
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                                                                                             Query Match
                                                                                                                                                                                                           SEQ ID NO 674
                                                                                                                                                        LENGTH: 449
TYPE: DNA
ORGANISM: Homo sapiens
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1233 cgctctgagctccattctccttcaagacctccccaacttcccaggttgaactacagcaga 1292
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                                                             Conservative
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99.3%;
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99.3%;
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                                                                Score 424.2; DB 19; Length 449; Pred. No. 6.1e-81;
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Pred. No. 6.1e-81;
0; Mismatches 3; Indels 0;
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CURRENT APPLICATION NUMBER: US/09/306,350A
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 41304
SOFTWARE: pt_CT_1 Version 1.1
SEQ ID NO 14682
LENGTH: 458
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-350A-14682
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APPLICANT: Drmanac, Radoje T.
APPLICANT: Jones, Lee W.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Prom Various cDNA Libraries
FILE REFERENCE: 20411-776
FILE REFERENCE: 20411-776
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280 GCAGAGCTTGGTGGGCGATGCCAAAGGAATACTGAAACCTTTAG-GTGTCCAGTCTGGAA
                694 gcagagottggtggacgatgccaaaggaatactgaaacctttagtgtgtccagtctggaa 753
                                                                               634 ttaatgtgttattaatgggttgaatctaattgggaagggagagagggttgcagagtgaggt
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                                                                                                                              GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGT-GGCTAAGCAAAGGGTTA
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APPLICANT: Jones, Lee W.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various cDNA Libraries
FILE REFERENCE: 20411-776
CURRENT APPLICATION NUMBER: US/09/909,629
CURRENT FILING DATE: 2001-07-19
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/306,350
PRIOR FILMS DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 41304
SOFTWARE: pt_CT_1 Version 1.1
SEQ ID NO 14682
LENGTH: 458
TYPE: DNA
TYPE: DNA
TYPE: DNA
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339 TTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGTGTGCAGAGTGAGGT 281
                                                              162 CATGCTAAACTACGTAAGAGCTATCTACCGTTCCAAAGCAATAG-GACTTTGAACAGTGT 104
                                                                                  814 catgctaaactacctaagagctatctaccgttccaaagcaatagtgactttgaacagtgt 873
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Search completed: September 7, 2002, 22:33:42 Job time: 43916 sec

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S-10-035-832-1262  S-10-011-154-674  S-10-011-154-674  S-10-013-154-477  S-10-143-966-21  S-10-035-832-1263  US-10-035-832-1263  US-10-035-832-1263  US-10-035-832-1269  US-10-031-872-1669  US-10-027-632-134015  US-10-027-632-253751  US-10-027-632-253751  US-10-027-632-253751  US-10-027-632-253751	pending_Factodata/2/pna/USO_NEW_COMB.seq: *  (cgn2_6/ptodata/2/pna/USO_NEW_COMB.seq: *  (cgn2_6/ptodata/2/pna/U	table:  1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1	col selic selic	us-09-834-291-3.rnpn us-09-834-291-3.rnpn 26 27 28 29 29 30
Matches  1 agctttttggctacatttttfattgtaagtaagtaagtacacacacacactactagagttgctggctataat 120  Qy  8441 agcttttttggctacattttttattgtaaggaagatccacacatatggagttgctggtgtgtgt	PRIOR APPLICATION NUMBER: 2010-03-02 PRIOR PILING DATE: 2001-03-02 PRIOR FILING DATE: 2011-03-02 PRIOR FILING DATE: 2011-03-03 PRIOR FILING DATE: 2011-03-1613 PRIOR FILING NOS: 1613 P	RESULT 035-832-1262 US-10-05-832-1262 US-10-06-1262, Application US/10035832  Sequence 1262, Application David Sequence 1262, Application David GENERAL INFORMATION ENGL COMPOSITIONS AND METHODS FOR CANCER APPLICANT ENGLAND SOCIETY OF THE OF INVENTION SUMBER: US/10/035,832  TITLE OF INVENTION NUMBER: US/10/035,832 FILE REPERENCE: A-7128-108-108-737 CURRENT APPLICATION NUMBER: US 09/747,377 CURRENT FILING DAVID SOCIETY OF THE OFFICATION NUMBER: US 09/747,377 CURRENT FILING DAVID SOCIETY OF THE OFFICATION NUMBER: US 09/747,377 CURRENT FILING DAVID SOCIETY OF THE OFFICATION SUMBER: US 09/747,377	2-179 2-179 2-11188 32-13188 32-1328 32-332 239-329 239-329 239-329 239-318-1404 9257-786 9257-786	\$\begin{array}{cccccccccccccccccccccccccccccccccccc

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GENERAL INFORMATION:
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11021 ctttcttcttttgccctttcttagcttgcactcccatggtgatttctggtctcctg 11080
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CURRENT FILING DATE: 2001-12-06

CURRENT FILING DATE: 2001-12-06

CURRENT FILING DATE: 2001-03-13

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/524,038

PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-13

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/404,284

PRIOR PRIOR PRIOR FILING DATE: 1999-09-21

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21

SOFTWARE: Hy Patent.pl Version 3.1

SEQ ID NO 674

LENGTH: 449

LENGTH: 449
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APPLICANT: Labat, Ivan
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Stache-Crain, Birgit
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similarity 99.3%; pred. No. 7.2e-81;
pred. No. 7.2e-81;
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Sequence 477, Application US/10211364
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/214,886
PRIOR PRILING DATE: 2000-02-04
PRIOR PRILING DATE: 2000-06-28
PRIOR PRILING DATE: 2000-06-28
PRIOR PRILING DATE: 2000-06-28
PRIOR PRILING DATE: 2000-07-11
PRIOR PILING DATE: 2000-07-11
PRIOR PRILING DATE: 2000-09-26
PRIOR PRILING DATE: 2000-07-26
PRIOR PRILING DATE: 2000-07-26
PRIOR PRILING DATE: 2000-07-26
PRIOR PRILING DATE: 2000-07-16
PRIOR PRILING DATE: 2000-07-17
PRIOR PRILING DATE: 2000-07-17
PRIOR PRILING DATE: 2000-07-17
PRIOR PRILING DATE: 2000-07-14
PRIOR PRILING DATE: 2000-07-14
PRIOR PRILING DATE: 2000-07-14
PRIOR PRILING DATE: 2000-07-14
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ16C1N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/760,486
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT
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                                                                                                                                                                                                                                                                                                                                                                  US-10-211-364-477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 1778
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                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: (594)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: misc_feature NAME/KEY: misc_feature LOCATION: (704)
                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: n equals a,t,g, or c
                                                              1477 ccccaacccgggcgttccccagcgaggcttccttcccatcctcctgaccaccggggcttt 1536
| 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 |
1537 tcgtgagctcgtctctgatctcgcgcaagagtgacacacaggtgttcaaagacgcttctg 1596
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                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                   10.0%;
                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                               Score 237.4; DB 6; Length 772; pred. No. 6.2e-41;
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PCT-US02-10824-85
                                                                                                                     RESULT
    Sequence 85, Application PC/TUS0210824

APPLICANT: OriGene Technologies

TITLE OF INVENTION: Prostate Cancer Expression Profiles

CURRENT APPLICATION UMBER: PCT/US02/10824

CURRENT FILING DATE: 2002-04-08
                                                                                    Sequence 85,
                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: n equals a,t,g, or c US-10-143-906-21
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                              Query Match
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0S-10-143-906-21
i Sequence 21, Application US/10143906
GENERAL INFORMATION:
                                                                                                                                1657 oggaacacacctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgg 1715
                                                                                                                                                                                 1597 gggagtgagggaagcggtttacgagtgacttggctggagcctcagggggcggggcactggca 1656
                                                                                                                189 cggaacacacctgaggccagccctggctgcccaggcggagctgcctcttctcccgcgg 247
                                                                                                                                                                                                                                 1537 tcgtgagctcgtcttgatctcgcgcaagagtgacacacaggtgttcaaagacgcttctg 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 772
                                                                                                                                                                   1477 ccccaacccgggcgttccccagcgaggcttccttcccatcctcctgaccaccggggcttt 1536
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CURRENT FILING DATE: 2002-05-14
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (704)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: (594)
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OTHER INFORMATION: n equals a,t,g, or c
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                   69 togtgagetegtetetgatetegegeaagagtgacacacaggtgtteaaagaegettetg 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: (593)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                    9 cgccaaccogggcgttccccagcgaggcttccttcccatcctcctgaccaccggggcttt 68
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238;
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                                                                                                                                                                                                                                                                                                                                              Conservative
2002-04-08
                                                                                                                                                                                                                                                                                                                                                      10.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
FILE REFERENCE: 49921-5068-WO
CURRENT APPLICATION NUMBER: PCT/US02/25766
PRIOR APPLICATION NUMBER: US 60/311,837
PRIOR APPLICATION NUMBER: US 60/311,837
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2010-08-14
PRIOR FILING DATE: 2011-08-14
PRIOR FILING DATE: 2011-0
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                             1681 tggctgcccaggcggagctgcctcttctcccgcgg 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US02-25766-9394
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                                                                                                             1621 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 1680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FAULK,
APPLICANT: SUN, F
APPLICANT: SASAI,
APPLICANT: WAGA,
APPLICANT: YAMAMO
121 tggctgcccaggcggagctgcctcttctcccgcgg 155
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GENERAL INFORM
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APPLICANT: GENE LOGIC, INC.
APPLICANT: MUNGER, William E
APPLICANT: FAULK, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US02-10824-85
                                                                            61 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 120
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Local .
155;
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PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/281,731
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1681 tggctgcccaggcggagctgcctcttctcccgcgg 1715
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                        ilarity 100.0%; Pred. No. 3.2
Conservative 0; Mismatches
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Similarity 100.0%; Score 155; DB 1; Length 2551;
55; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SASAI, Hitoshi
WAGA, Iwao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application PC/TUS0225766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hongwei
                                                                                                                                                                                                                                                                                                                              6.5%; Score 155; DB 1; Length 2551; 100.0%; Pred. No. 3.2e-23;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels 0; Gaps
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APPLICANT: ENGLISH FOR CANCER APPLICANT: ENGGENATOR ENGGENATOR AND METHODS FOR CANCER TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER TITLE OF THE PRIOR APPLICATION NUMBER: US/10/035,832

CURRENT FILING DATE: 2002-07-22

PRIOR FILING DATE: 2001-12-2

PRIOR FILING DATE: 2000-12-2

PRIOR FILING DATE: 2000-13-9

PRIOR FILING DATE: 2000-13-9

PRIOR FILING DATE: 2000-13-9

PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 1613

SEQ ID NO 1263

SEQ ID NO 1263

LENGTH: 2551
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Sequence 1263, Application US/10035832
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MOTILS, David
APPLICANT: Engelhard, Eric
APPLICANT: Engelhard, COMPOSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-832-1263
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Sequence 143, Application US/10007926A
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 143
SEQ ID NO 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BERTUCCI, FRANCOIS
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES FILE REFERENCE: 1546-R-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VIENS, PATRICE APPLICANT: FERT, VINCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1561 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgaggggaagcggtttacga 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1621 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1681 tggctgcccaggcggagctgcctcttctccccgcgg 1715
                                                                                                             OTHER INFORMATION: tumor necrosis factor receptor superfamily, OTHER INFORMATION: member 6 (TNFRSF6) gene.
                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 tggctgcccaggcggagctgcctcttctcccgcgg 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 gtgacttggctggagcctcaggggcgggcactggcacggaacacaccctgaggccagccc 120
                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
                                                                                                                                                                                                                                          2551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOULGATTE, REMI
BIRNBAUM, DANIEL
NGUYEN, CATHERINE
            100.0%;
                                 6.5%;
          Score 155; DB 7;
pred. No. 3.2e-23
                                           Length 2551;
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-053-375B-233
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CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 233
LENCTH: 2534
                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-10-035-832-1259
                                                                                                         CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
5.4%; Score 129; DB 5; Length 2534;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 129; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                        ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvilli, Robert
TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CLON-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1561 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgaggggaagcggtttacga 1620
                                                                                                                                                                                                                                                                                                                                                          sequence 1259, Application US/10035832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1621 gtgacttggctggagcctcaggggcgggcactggcacgggaacacaccctgaggccagccc 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1681 tggctgcccaggcggagctgcctcttctccccgcgg 1715
                                                                                            SOFTWARE: Pate
SEQ ID NO 1259
                                                                                                                                                                                                                                                               APPLICANT: MOTRIS, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 tggctgcccaggcggagctgcctcttctcccgcgg 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1707 ctcccgcgg 1715
                                                         TYPE: DNA
                                                                        LENGTH: 55996
NAME/KEY: misc_feature
                    FEATURE:
                                     ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ctcccgcgg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR TILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-035-832-1259
PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 68.2; DB 6; Length 55996; Best Local Similarity 63.6%; Pred. No. 0.00024; Matches 152; Conservative 0; Mismatches 83; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  7917 agacttotottttttgatagatttatatootgaotatggtoocotaactottttoaccoc 7975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7859 aag-gaggaagtaataatgtot-aacacagcaggtgagggttttccccttttactgaaaat 7916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (55549)..(55568)
OTHER INFORMATION: "n" at positions 55549 thru 55568 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7799 cagtaaagaagtataagaatttittttaacgaaaattggtcaggaaataatccgtaacaa 7858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (53136)..(53155)
OTHER INFORMATION: "n" at positions 53136 thru 53155 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   943 aggacaggaagtaattgtgaatgtttaatatagctggggctatgcgatttggcttaagtt 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (50692)..(50711)
OTHER INFORMATION: "n" at positions 50692 thru 50711 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   883 cacgaaagaattacaagatttttttttaaagaaaattggccaggaaataatgagtaacga 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (48271)..(48290)
OTHER INFORMATION: "n" at positions 48271 thru 48290 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (50692)..(507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            825 acctaagagctatctaccgttccaaagcaatagtgactttgaacagtgttcacca--gag 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: (48271)..(48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (46987)...(47006)
OTHER INFORMATION: "n" at positons 46987 thru 47006 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (42691)..(42710)
OTHER INFORMATION: "n" at positions 42691 thru 42710 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (31023)..(31239)
OTHER INFORMATION: "n" at positions 31023 thru 31239 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (29253)..(29272)
OTHER INFORMATION: "n" at positions 29253 thru 29272 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: (31023)..(31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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US-10-113-872-1669/c
; Sequence 1669, Application US/10113872
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-10-113-872-796
                                                                         APPLICANT: Watanabe, Yoshihiro APPLICANT: Henderson, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.5%;
Best Local Similarity 69.8%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                     APPLICANT:
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                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Human
US-10-027-632-145670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 796, Applic GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 2011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/113,872 CURRENT FILING DATE: 2002-03-28
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C19
                                                                                                                                                                                                                                                                                                               2374 TAGATTTAGAGAGAAGTTGGAGAGATAGTAGAAAGAGTTGCTGTATAGCCCTTCAGC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               2434 Trititititititititititititititaaattaaataaactitiatititiggaatgatac 2375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Watanabe, Yoshihiro
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 145670
LENGTH: 816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2435
                                                                                                                                                                                                                                                                                                                                                       289 taggatttcaaaaaatttgcagagataatacagagaatgcccatataccatcctcc 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 ttttccttccttcttttacattttttatttaaatgaacttttcattttggaatagttt 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 gagataatacagagaatgcccatataccatcctccttatcccacttctttttgtgtctat 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 AÁGATAGTACAGAAAATTCCCACATACTGCACACCGTTTCCCCCTGTTTTTAACATTTTAT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 TGTTTTTGTTTAAATAAACTTTTGCTTTTAGAACAGTTTTAGCTCTACAGAATTATTGCA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 tttttttatttaaatgaacttttcattttggaatagttttaggatttcaaaaaatttgca 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match
Local Similarity 69.2%; Pred. No. 0.0031;
hes 83; Conservative 0; Mismatches 37; Indels
Henderson, Robert
Kalos, Michael D.
Sleath, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 4.0
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Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Henderson, Robert
Kalos, Michael D.
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                                                                     Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60; DB /; Pred. No. 0.0061; No. 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7; Length 2435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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; TYPE: DNA; ORGANISM: Homo sapiens
US-10-113-872-1669
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US-10-027-632-91808
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1669
LENGTH: 2821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CATTET, DATFICK
APPLICANT: FANGER, GATY R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.478C19
CURRENT APPLICATION NUMBER: US/10/113,872
CURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                                                    ; ORGANISM: Human
US-10-027-632-91808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 91808, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome TILE REFERENCE: 108827.129
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 91808
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR TILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                       Query Match
Best Local Similarity
Matches 70; Conserv
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                                                                                                                                                                                                                                                                                   TYPE: DNA
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Local Similarity 69.8%; Pred. No. 0.0063; |
Local Similarity 69.8%; Pred. No. 0.0063; |
Nes 81; Conservative 0; Mismatches
                                                       310 gagataatacagagaatgcccatatacc 337
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                                                                                                                                                              2.5%;
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US-10-027-632-304597
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 304597
LENGTH: 542
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
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PRIOR EILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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PRIOR FILING DATE: 2000-03-29
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Search completed: September 8, 2002, 01:12:00 Job time: 37198 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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AA058275 zf53g03.s
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AA018441 ze50a08.s
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## ALIGNMENTS

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zj19h02.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:450771 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
Seq primer: -40m13 fwd. ET 459.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:1387127"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:450771"
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 793)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                     Contact: Robert Strausberg, Ph.D
                                                                                                                                                                Eukaryota;
                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                               603049567F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189752 5',
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Similarity 99.8%;
Sequencing by: Incyte Genomics, Inc.
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                                                                                                                                                                                                      92 TCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTCATTTTGTTTTTGTTTTTCTGCCCT 33
                                                                                                                                                                                                                                                                                                                                                                                                          272 CTCAGACGTAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCCGGAGGGCCTCGGAAGAA 213
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                                  AA058563 603 bp mRNA linear EST zf55b04.sl Soares retina N2b4HR Homo sapiens cDNA clone
AA058563.1 GI:1551370
                         IMAGE:380815 3', mRNA sequence
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Tel: 314 286 1800
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Fax: 314 286 1810
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//dev_stage="55 year old"
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/clone_lib="Soares retina N2b4HR"
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Contact: Wilson RK
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Soares and M.Fatima Bonaldo. "

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/db_xref="GDB:1288949"
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                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 442)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ze34d02.sl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360867 3', mRNA sequence.
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                                                                     /dev_stage="55 year old"
                                                                                                                                                                                                                                                                               /tissue_type="retina"
                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                     /clone_lib="Soares retina N2b4HR"
                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:360867"
                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:1277412"
                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
     12.0%;
                                                                                                                                                                                                                                                                                                                                                                                       on/Qualifiers
Score 286.4; DB 9
Pred. No. 3.2e-41;
                                                                  103 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442 bp
                                                                  138 t
        DB 9; Length 442;
                                                              2 others
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FEATURES
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GTACTCGTTCCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCC 240
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                                                                                                                                                                                                                         Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, S., B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Scares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Generation and analysis of 280,000 human expressed sequence tags of 280,000 human expressed sequence tags.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTG
                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA047220 547 bp mrNA linear EST zf49e11.51 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380300 3', mrNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                  314 286 1800
314 286 1810
modified polylinker; Site_1: Not I; Site_2: Eco RI;
          /tissue_type="retina"
/dev_stage="55 year old"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye: Vector: pT7T3D (Pharmacia) with a
                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:1288557"
/db_xref="taxon:9606"
/clone="IMAGE:380300"
                                                                                                 /sex="male"
                                                                                                     /clone_lib="Soares retina N2b4HR"
                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                           AUTHORS
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A44/ DP MKNA LINEAL TO Zf59h03.sl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381269 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                   Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                           Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                              Unpublished (1995)
                                                                                                                                                                                                                               The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      AA057418.1 GI:1550059
                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) fon further information.
Seq primer: -40M13 fwd. from Amersham
                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                         High quality sequence stop: 339.
Location/Qualifiers
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             /organism="Homo sapiens"
/db_xref="GDB:1289526"
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                                                                                                                                                                          St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2201 ccctttcttagcttgcactcccatggtgatttct-gcttggtctcctgctggggttggtg 2259
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Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Clsh, W., Hawkins Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Clsh, W., Hawkins M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Le, N., Mardis, E., B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., B., Morris, M., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a /note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primer [5', str
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hes 277;
                    104209
ys95e09.s1 Soares retina N2D5HR Homo sapiens cDNA clone
IMAGE:222568 3', mRNA sequence.
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Fax: 314 286 1810
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/db_xref="taxon:9606"
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99.6%;
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                   2291 ctattattggccaagaaacttgagcagcctgttttgaaaagtccctcgctcagaaatgcc 2350
                                                                                             2231 ttetgettggteteetggtgggttggtggtactegtteeeacegcacagaaceeggege 2290
                                                                                                                                                                     2171 tgtttttetgeeettetetttettettetttgeeetttettagettgeaeteceatggtgat 2230
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181 CTATTATTGGCCAAGAAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCC 240
                                                                         121 TICTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTTCCCACCGCACAGAACCCGGCGC 180
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Location/Qualifiers
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washu-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 881 Std Error: 0.00
Seq primer: Promega -21m13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the LMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Source: IMAGE Consortium,
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Fax: 314 286 1810
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
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91 c 91 g 119 t
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/dev_stage="55 year old"
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/db_xref="GDB:3851329"
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                                                                                                                                                                                                                                                                                                        11.3%; Score 270; DB 10; 100.0%; Pred. No. 2.7e-38; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              Length 376;
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                                            2106 gtctcccttccgggaattctctctttaagactgtaagtcgctgc¢tgagtggtttcattt 2165
                                                                                                                                                                                          Local Similarity
H86126
ys94g08.s1 Soares retina N2b5HR Homo Sapiens CDNA clone
IMAGE:222494 3', mRNA sequence.
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The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stops: 378
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 925 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
                                                                                                                                                        270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 398)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 925
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/clone="IMAGE:222494"
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/db_xref="GDB:3851255"
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/lab_host="DH10B (ampicillin_resistant)"
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                                                                                                                                                                                          Score 259; DB 10;
Pred. No. 2.4e-36;
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AA018441
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The WashU-Merck EST Project
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Hillier, L., Clark, N., Dubuque, T., Elliston, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
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   59 a
   /tissue_type="retina"
//dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="Corrected Rise of the lighted to Rise of the lighted to Eco Rise of the local condition of
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/clone="IMAGE:362390"
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/db_xref="GDB:1279093"
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CTCGTTCCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCTGT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 10.7%;
Local Similarity 99.6%;
                                                                                                                                                                                                                                                                                    High quality sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 381)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
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The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
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381 bp mRNA linear EST yt04f01.s1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:223321 3', mRNA sequence.
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/tissue_type="retina"
/dev_stage="55 year old"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:223321"
                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:3854355"
                                                                                                                          /sex="male"
                                                                                                                                      /clone_lib="Soares retina N2b5HR"
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Pred. No. 1.6e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2231 ttctgcttggtctcctgctggggttggtggtactcgttcccaccgcacagaacccggcgc 2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2111 ccttccgggaattctctctttaagactgtaagtcgctgcctgagtggtttcatttttgttt 2170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AGCTTGCAGATGGGCTAATCAAAGGAGG 268
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mes 259; Conserv
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                                         Email: est@watson.wustl.edu
Insert Size: 958
High quality sequence stops: 269
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 958 Std Error: 0.00
              Insert Length: 958 Std Error:
Seq primer: Promega -21m13
High quality sequence stop: 269
                                                                                                                                                                                                                                                                ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                               Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 419)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "

3 others
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                                                                                                                                                                                                                             Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2363 gctaatcaaagagacgtg 2380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           696 bp mRNA |linear EST 11-OCT-2
AV715411 DCB Homo sapiens cDNA clone DCBAUÇ01 5', mRNA sequence.
AV715411
                        Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
251 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                   ,G., Cheng,Z. and Han,Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 696)
Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: hanzg@chgc.sh.cn
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/db_xref="GDB:3798432"
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/dev_stage="55_year old"
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/clone="IMAGE:274746"
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Pred. No. 2.6e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 828 bp mRNA linear EST 04-OCT-2001 603083875F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222802 5', mRNA securence
                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence
                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                           High quality sequence stop: 813
                                                                                                                                                                                               http://image.llnl.gov
Plate: LLAM11560 row:
                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 828)
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141 c 156 g 189 t
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/lab_host="BM25.8"
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/db_xref="taxon:9606"
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/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo
                                                                    /db_xref="taxon:9606"
/clone="IMAGE:522802"
/clone_lib="NIH_MGC_120"
                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                          cocation/Qualifiers
                                                       /lab_host="DH10B"
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87.8%;
                                                                                                                                                   . 828
                                                                                                                                                                                                    row: f column: 19

 Mismatches

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Pred. No. 3.2e-23;
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Search completed: September 7, 2002, 14:51:47 Job time: 16206 sec
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                                                                                                                                                                                                                                                   2139 taagtogotgootgagtggtttcattttgtttttgtttttctgccc 2183
                                                                                                                        181 TTCTTACGTCTGTTGCTAGATTATCGTCCAAAAGTGTTAATGCCC 225
                                                                                                                                                                                                                                                                                                                                                                                                         male. Library is oligo-dT primed and directionally cloned (ECORY site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
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Sequence:
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Result
No.
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  Score
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720
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Listing first 45 summaries
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Match Length DB
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6.2 71172
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6.1 173724
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6.1 175125
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6.1 105585
6.0 126985
6.0 128995
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AC106368
AL136314
AC102988
AP003267
AC013603
AC013603
AC024313
AC073582
AC108683
AC108683
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AC094291
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  AC098645
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AC109745
AC018798
AC097703
AL138904
AL157935
AC073750
HSU88351
HS1141019
AC094925
AC073151
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AC024561
AL160392
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AX026092 Sequence
AX026102 Sequence
AJ011034 Homo sapi
G27038 SHGC-30908
AJ279011 Homo sapi
AJ279013 Homo sapi
AJ279013 Homo sapi
AJ279013 Homo sapi
D31968 Human DNA f
AF429315 Homo sapi
166494 Sequence 14
AP004479 Lotus jap
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AC091283 Mus muscu
                 AJ224121 Canis fam
AJ224121 Canis fam
AJ224121 Canis fam
AC106368 Rattus no
AL136314 Human DNA
AC102988 Rattus no
AP003267 Cryza sat
AC013603 Homo sapi
AL1445675 Human DNA
AC024313 Homo sapi
AC106682 Homo sapi
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AC106682 Homo sapi
AC106694 Sequence 14
AC036124 Homo sapi
AC024561 Homo sapi
AC160392 Human DNA
AL59679 Homo sapi
AC197458 Homo sapi
AC197458 Rattus no
AC108798 Homo sapi
AC197703 Rattus no
AC138904 Homo sapi
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         AC073151 Mus muscu
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## ALIGNMENTS

IGIN	source	ATURES	JOURNAL F	OTHORS M	ERENCE 1	NISM	WORDS h		INITION S	90	ULT 1
	/ors	Location/Qualifiers	PATENT: DE 19847779-C 2 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE)	Mueller-Schilling, M., Alammeri, and Apoptosis-modulating Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy	1 (bases 1 to 720)	Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.	human .	AX026090 AX026090.1 GI:10187521	2 from Patent DE	720 bp DNA linear PAT 16-SEP-2000	

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FEATURES
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1 (bases 1 to 3212)

Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dha useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy

Patent: DE 19847779-C 1 03-FEB-2000;

DEUTSCHES KREBSFORSCH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATT
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                                                                                                                       Homo sapiens
                                                                                                                                                                     Sequence 1 from Patent DE19847779.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 100.0%; Score 720; DB 6; Length 720;
Similarity 100.0%; Pred. No. 1.4e-158;
20; Conservative 0; Mismatches 0; Indels
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                                                                                     complete sequence.
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3040 CCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 187313)
                                                                                                                                            Human DNA sequence from clone RP11-399019 on chromosome 10,
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/db_xref="taxon:9606"
/84 c 809 g 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 144529 GAGGTGGGGTGGGGTGCGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC
                                                                                                                                                                               Db 144589 TGGAGGGGGACCCCGGTTGGAGAGAGGAGGGGAACTCCTGGACAAGCCCTGACAAGCCAA 144648
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                                                                                                                                                                                                                                       121 tggagggggaccccggttggagagagggagctcctggacqagccctgacaagccaa 180
                                                                                                                                                                                                                                                                                                                                                                                                    61 gaggtgggggggggggggacaggaattgaagcggaagtctggggaagctttagggtcgc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 0.00); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least as compressions or more than one MI3 subclone; and the one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following assembly was confirmed to associate primary accession numbers given in the feature table with their source databases: Em: NMEL; Sw:, proposed to the confirmed 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. |
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 purple information can be found at mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/HGP/Chr10

RP11-399019 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the entire insert of clone RP11-399019 The true left end of clone RP11-496H23 is at 166408 in this sequence. The true right end of clone RP11-304I5 is at 18704 in this sequence.
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/note="Sequence confirmed by AC015461 sequenced by WIBR."
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/note="Sequence from AC015461 sequenced by WIBR."

105973. .105989
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/clone="RP11-399019"
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Pred. No. 7.1e-157;
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Db 145069 TACTCGTTCCCACCGCACAGAACCCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCT 145128
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AX026091
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                                            106 aagetttagggtegetggaggggaeceeggttggagagaggageggaaeteetggaeaa 165
226 gcgggggcgggggagagagcctacagccttcagaacacatattgctcattttctggcagtt 285
                                                          166 gccctgacaagccaaagctcaaaggtccgctccggcgcgggttgggttgagttgcgcgccgcccc 225
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1 (bases 1 to 2380)
Mueller-Schilling,M., Krammer,P. and Oren,M.
Mueller-Schilling,M., Krammer,P. and Oren,M.
Movel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy patent: DE 19847779-C 3 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
595 c 568 g 638
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99.7%;
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1 (bases 1 to 2827)

Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy

Patent: DE 19847779-C 4 03-FEB-2000;

DEUTSCHES KREBSFRSCH (DE)
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/db_xref="taxon:9606"
676 c 657 g 766
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61 GAGGTGGGCGTGGGGGGGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC 120
                61 gaggtgggcgtggggggggggacaggaattgaagcggaagtctggggaagctttagggtcgc 120
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                                                                                 1 gatcccgctgggcaggcggggcagctcccggcgctcctcggagaccactgcgctccacgtt 60
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1 (bases 1 to 266)
Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 32 03-FEB-2000;
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72 c 110 g
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                                                                                                                                                          36.5%;
99.2%;
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Pred. No. 2.7e-51;
0; Mismatches 2;
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Query Match Best Local 9

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241 gagcctacagccttcagaacacatat 266
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                                                   121 TGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACTCCTGGACAAGCCCTGACAAGCCAA 180
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                         241 gagcctacagccttcagaacacatat 266
                                                                                                                                                                                            Homo sapiens DNA for enhancer of CD95 gene, AJ011034
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 266)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD95 gene; enhancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-SEP-1998) Mueller M., Department of Internal Medicine IV, University Hospital, Bergheimerstr. 58, Heidelberg, 69115,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mueller,M., Wilder,S., Bannasch,D., Israeli,D., Lehlbach,K.,
Li-Weber,M., Friedman,S.L., Galle,P.R., Stremmel,W., Oren,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mueller, M
                                       tggagggggaccccggttggagagaggggggaactcctggacaagccctgacaagccaa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53 activates the CD95 (APO-1/Fas) gene in response to DNA damage
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                     /gene="CD95"
159. .178
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                      /gene="CD95"
                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:4165483
                                                                                                                                                                                                                                                                   36.5%;
                                                                                                                                                                                                                                                                                                                                   72 c
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                                                                                                                                                                                                                                                               Score 262.8; DB 9;
Pred. No. 2.7e-51;
C. Mismatches 2;
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398 bp DNA linear STS 30-MAR-2
SHGC-30908 Human Homo sapiens STS genomic, sequence tagged site.
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Olivier, M. and Cox, D.R. (2000)
Unpublished, Olivier, M., Cox, D.R. (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: (650) 320-5800
Fax: (650) 320-5801
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Email: olivier@shgc.stanford.edu
Primer A: GTCTCCCTTCCGGGAATTCT
Primer B: AACCCCAGCAGGAGACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Michael Olivier, David R. Cox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pcR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protocol
                                                                                                 270;
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                                                                                                             Similarity
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                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial incubation: 94 degrees C for 90 seconds
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93 c 105 9
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                              /clone_lib="Human"
                                                                                                                 36.0%;
99.6%;
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pred. No. 2e-50;
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                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muschen, M.
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Muschen,M., Re,D., Brauninger,A., Wolf,J., Hansmann,M.L., Diehl,V., Kuppers,R. and Rajewsky,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Muschen, M., Re, D., Jungnickel, B., Diehl, V., Rajewsky, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Apo-1 Fas; CD95 antigen; CD95 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 702)
                                                                    /product="CD95 antigen"
/protein_id="CAC35540.1"
/db_xref="GI:13539241"
                                    /gene="CD95"
                                                      /translation="MLGIWTLLPLV"
                                                                                                                                                              /gene="CD95"
/standard_name="Apo-1 Fas"
282. .>313
                                                                                                                        /standard_name="Apo-1 Fas'
                                                                                                                                               /gene="CD95"
                                                                                                                                                                                                         /number=1
<1. .281
                                                                                                                     /codon_start=
                                                                                                                                                                                                                     /standard_name="Apo-1 Fas"
                                                                                                                                                                                                                                                                                                   /Organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="Reed Sternberg cells"
                                                                                                                                                                                                                                             /gene="CD95"
                                                                                                                                                                                                                                                                        /gene="CD95"
                                                                                                                                                                                                                                                                              /note-"Hodgkin's disease tissue-polymorphic allele (+275)"
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                     Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931
                                                                                                                                                                                                                                                Related sequences: D31968 x89101 AJ279012 AJ279013.
                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                      Muschen, M.
                                                                                                                                                                                                                                                                                                                                                                      Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
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Muschen,M., Re,D., Brauninger,A., Wolf,J., Hansmann,M.L., Diehl,V.,
Kuppers,R. and Rajewsky,K.
                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Muschen, M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
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      /standard_name="Apo-1 Fas"
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/codon_start=1
                            /gene="CD95"
                                        /gene="CD95"
/standard_name="Apo-1 Fas"
282. .>313
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                                                                                                                          /gene="CD95"
                                                                                                                                                                      /cell_type="Reed-Sternberg cells"
/note="Hodgkin's disease tissue"
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/db_xref="taxon:9606"
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100.0%; Pred. No. 2.1e-24;
tive 0; Mismatches 0;
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Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas),
1, polymorphic allele (+337).
AJ279013
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Muschen,M., Re,D., Brauninger,A., Wolf,J., Hansmann,M.L., Diehl,V., Kuppers,R. and Rajewsky,K.

Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
                                                                                                                                                                                                                                                                                                                                                    Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction
                                                                                                                                                                                                                                                                                                                                                                                         muschen, M., Re,D., Jungnickel,B., Diehl,Vi, Rajewsky,K. and
                                                                                                                                                                                            submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9,
                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                     Related sequences: D31968 X89101 AJ279011 AJ279012
                                                                                                                                                                                                                                   Muschen, M.
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/db_xref="GI:13539239"
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    /number=1 <1. .281
                                                                                           /dblxref="taxon:9606"
/call_type="Reed-Sternberg cells"
/note="Hodgkin's disease tissue-polymorphic allele (+337)"
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                                                                /gene="CD95"
                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                         ocation/Qualifiers
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                           /standard_name="Apo-1 Fas"
                                         /gene="CD95"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2165)
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                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28 JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:nakanaka@dbs.p.kanazawa-u.ac.jp, Ishikawa 920-0934, Ishikawa 920-093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection Biol. Chem. 270 (30), 18007-18012 (1995)
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/db_xref="GI:13539243"
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                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
            /bound_moiety="NF-IL6"
772. .780
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                                                                                                                                                                                                             /tissue_type="blood"
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                                                                                              /bound_moiety="NF-IL6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocal Similarity
                                                                                                                                                          Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 125020)
Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Potter, N.T., Ross, C.A. and Margolis, R.L.
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 (4), 377-378 (2001)
                                                                                                                                                                                                                    Holmes, S.E., Inger
Direct Submission
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HOMO Sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
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/gene="JpH3" .>36887)
                                         /note="isolated from a patient with Huntington's Disease-Like 2 (HDL2)" complement(35581. .35746)
                                                                                                            /Organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
                                       /rpt_type=tandem
                                                                                      /map="16q24.3; between D16S520 and WI-12410"
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1814. .>2165
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/protein_id="BAA20850.1"
/db_xref="GI:4433150"
                           _unit=ctg
                                                                                                                                                                                                                Ingersoli-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
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99.1%;
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Pred. No. 2.2e-15;
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                                                                                                51377 MTRSCTCMGMCTCCT8MSKRGYTSRSRCYAYWSKCSYSYSYCMRCCW 51423
                                                                                                                                                                 51317 YKRWGKCTCRMWSWRKWRGCMGSAGGGSWRGAKYSMMSTSKYGSRWTCWMRSCWYWCTSC 51376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
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                                                                                                                                                                                                                                                                                                          51197 GRWGKATRWTRTRSSSRMSWYYKYAWMMRRWTTAGKKWKTKTTWSTKKKSKWGRMYRSRW 51256
                                                                                                                                                                                                                                                                                                                                                                              51137 AWWYSMCCSKCARAASGWYKCMMMKGGCYYGGGKGSASTWMYMMCCSRACKYYTTRKSSR 51196
                                                                                                                                                                                                                                                                                                                                                                                                                                                51077 CSCCMRCSWYCWYKCMRYGSWRMYKCCMSYKTCKYKGCSATKSMAMYYSCMRWRKGTKSS 51136
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                                                                                                                                  614 cgcacagaacccggcgcctattattggccaagaaacttgagcagcct 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51017 WGAGRSSRYCKSGSRMSMAGGSMSASMSMGKMTSGMSGRCCARSGRMSAYCSCRKCKSKR 51076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50897 MHRKKHYKKDSHBSWGKSHMKKGAWRVRSMYRSMRCSVHDSSMVDKSRRRMKGSAMRGMK 50956
                                                                                                                                                                                                 554 tgcactcccatggtgatttctgcttggtctcctgctggggttggtggtactcgttcccac 613
                                                                                                                                                                                                                                                                       434 ggaaactgccttgtctcccttccgggaattctctctttaagactgtaagtcgctgcctga 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50837 VRBSSMKCSRRKDMSTSSMWRSMKDRKCSRCSHSHYSKSMGKWTSDVDRCYACSSBMKYK 50896
                                                                                                                                                                                                                                                                                                                                                                                                          374 tatgggggctgaatgagcttctggaggcttgtttaccgtttttttattgtcacacagaaaa 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 tcagaacacatattgctcattttctggcagttctcagacgtaggaaataagtcagcaccg 313
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Local Similarity 12.4%; Pred. No. 0.0032;
hes 80; Conservative 293; Mismatches 269; Indels 5
 Sequence 14 from patent US 5670367.
I66494
                                    166494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSSGGRFNPDDGGSYCGGWEDGKAHGHGVCTGPKGOGEYTGSWSHGFEVLGYYTWPSGNTYQGTWAQGKRHGTGLESKGKWYKGEWTHGFKGRYGVRECAG NGAKYEGTWSNGLQDGYGTETYSDG"
29056 a 32731 c 30696 g 28283 t 4254 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="junctophilin 3"
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/db_xref="GI:17646245"
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/gene="JPH3"
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complement(<36507. .>36887)
/gene="JPH3"
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               linear
       PAT 28-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 attotototttaagaotgtaagtogotgootgagtggtttoattitgtttttgtttttotg 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641 ccaagaaacttgagcagcctgttttgaaaagtccctcgctcagaaatgccag 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               581 teteetgetggggttggtggtaetegtteecacegcacagaaceeggegeetattattgg 640
                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 7218)
Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I66494.1 GI:2724471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP004479 41820 bp DNA | linear PLN 14-DEC-2001 Lotus japonicus genomic DNA, chromosome 1, clone:LjT03H13, TM0012b,
                                                                    Submitted (13-DEC-2001) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail ynakamu@kazusa.or.jp, URI:http://www.kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                             Sato,S., Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T. and Tabata,S. Structural Analysis of a Lotus japonicus Genome. I. Sequence Features and Mapping of Fifty-six TAC clones which cover the 5.4 Mb Regions of the Genome
                                                                                                                                                                                                                                                                                                                                                                                                                   Lotus japonicus DNA, clone_lib:LjT library clone:LjT03H13.
Lotus japonicus
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/organism="Lotus japonicus"
/db_xref="taxon:34305"
                                                        Location/Qualifiers
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29577 GACTTTATTCAGGTAAATAAGGTGATGCATGCCCCATTACATTTTCTTTTCTTTTCTCTC 29518
                                                                    29637 TIGITITCTCTCTTTACTTTACAAACAGCAAATAAAAATAAACATTTTCCATAAATGAAA 29578
                                                                                          402 ttgtttaccgttttttattgtcacacagaaaaggaaactgccttgtctcccttccgggaa 461
                    13734 a
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                 /clone="LjT03H13"
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/note="TM0012b, a part of TAC clone:TM0012"
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                                                                                                                                                                                                                                                                                                                    /chromosome="1"
                                                                                                                                                              58.6%;
                                                                                                                                               0; Mismatches
                                                                                                                                                              Score 47.6; DB pred. No. 0.56;
                                                                                                                                                                                  DB 8; Length 41820;
                                                                                                                                                 69; Indels
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Search completed: September 7, 2002, 18:26:31 Job time: 29090 sec

29517 TGACCCCCTCTTTCTCTCTCACTTGCATAGGTTCCTTTCACTGTATCTTTT 29464

519 tgcccttctcttcttcttttgccctttcttagcttgcactcccatggtgattt 572

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1: /SIDSI/gcgdata/h
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT:*
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/SIDS1/gcgdata/hold-genesed/genesedn-embl/NA2001A.DAT:*
/SIDS1/gcgdata/hold-genesed/genesedn-embl/NA2001B.DAT:*
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AAI91235
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AAI82334
AAI92484
                              AAI85304
AAI83979
           AA189184
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try)		266		23	22	22	22	163	) K	22	22	22	19	1 C	) k	2 2	22	22	22	22	22	2 6	) N	) N	22	22	22	22	22	22	22	20	22	22	22	22
		вр.	ALIGNMENTS	AAH88704	9	AA188083	AAI91417	AAS/82/2	AAL93364	AAI83890	AAI83384	AAI92134	AAV57903	ARI.33718	AA166052	AAS86364	AA192211	AAS35779	AAI85356	AA189117	AA187907	AAS35104	AA104000	AA549/00	ABAU5830	AAI83697	AAD16391	AA191277	AA185354	AA183837	AAI88050	AAZ17263	AAI92479	AA189131	8138	AAS44777
				nullian pass segment	JNA	Human porynuciecci	Human polynucleoti	re	=	Human polynucleoti			-	Human immune syste		Human polynucleoti	num encoding novel	Human carurouscur			Human polynucleoti	5	Human DNA for a no			Human denomic DNA		Monse interferon i		nullan polymertore			роту	n	Human polynucieoti	

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Key
                                                                                                            p53; CD95 receptor; human; screening; apoptosis-modulation;
cancer chemotherapy; ss.
                                                                                                                             Human CD95 receptor intron 1 fragment.
                                                                                                                                        11-MAY-2000
                                                                                 protein_bind
                                                                                                  Homo sapiens
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                                                                                  Location/Qualifiers 160..179
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03-FEB-2000. DE19847779-C1.

98DE-1047779. 98DE-1047779

/bound\_moiety= p53

/\*tag=

Krammer P,

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

Mueller-Schilling M, Oren M;

16-OCT-1998; 16-OCT-1998;

WPI; 2000-162245/15

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AAI84123/c
ID AAI841
XX AAI841
XX AAI841
XX DT O6-NOV
XX Human;
KW Human;
KW vaccin
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   WPI; 2001-514838/56
                                                     Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                       28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; humunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                  26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 gagcctgcagccttcagaacagatat 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 gaggtgggcgtgggggggacaggaattgaagcggaagtctgggaagctttagggtcgc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gatcccgctgggcaggcgggcagctccggcgctcctcggagaccactgcgctccacgtt 60
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99.2%;
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Pred. No. 7.5e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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             Tang YT,
                                          (HYSE-) HYSEQ INC.
                                                                                         28-FEB-2000;
                                                                                                                                                        07-SEP-2001
                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                           18-MAY-2000;
                                                                                                                     26-FEB-2001; 2001WO-US04927.
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                                                                                                                                                                                                                       HOMO sapiens.
                                                                                                                                                                                                                                                                                                                             Human polynucleotide SEQ ID NO 11295
                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               AAI91235
                                                                                                                                                                                                                                                                                                                                                                                                                        AAI91235 standard; cDNA; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, estimated the prowth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity, insunomodulatory activity and treatment of cancer, leukaemia, nervous system disorders, arthritis and treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 428 BP; 203 A; 48 C; 92 G; 82 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532 cttctttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctg 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        472 aagactgtaagtcgctgcctgagtggtttcatttttgtttttgtttttctgcccttctcttt 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 ttttttattgtcacacagaaaaggaaactgocttgtctccctttccgggaattctctcttt 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4183; 1399pp + Sequence Listing; English
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          Liu C,
                                                                        2000US-0515126.
2000US-0577409.
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          Drmanac RT;
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Pred. No. 0.0006;
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hes 82; Indels
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2001-514838/56.

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 11295; 1399pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                        06-NOV-2001 (first entry)
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tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy;
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                                                                                                                                                                         nervous system disorders; arthritis; inflammation;
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   28-FEB-2000;
18-MAY-2000;
                                              26-FEB-2001; 2001WO-US04927.
                                                                                                               WO200164835-A2
                                                                                                                                             Homo sapiens
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   2000US-0515126.
2000US-0577409.
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51.7%;
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Pred. No. 0.0015;
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AATB2334/c
ID AATB23
XX
AC AAIB23
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AC Human
DE Human
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KW Human
KW Vaccit
KW tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 2337; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 386 BP; 213 A; 30 C; 52 G; 72 T; 19 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iagnosing and treating e.g.
                                                                                                                                                                                                                                                                                                                                               AAI82334 standard; cDNA; 423 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 ttttttattgtcacacagaaaaggaaactgccttgtctcccttccggggaattctctcttt 471
                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                  06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                AAI82334;
                                                                                                                                                                                                                                                                                                                                                                                                                               472 aagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctcttt 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polynucleotide SEQ ID NO 2394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             532 cttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcctg 587
                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                              26-FEB-2001; 2001WO-US04927.
                                                                                                 WO200164835-A2
 28-FEB-2000; 2000US-0515126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia, inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45.6; DB 22; Length 386; pred. No. 0.0037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and immune
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18-MAY-2000; 2000US-0577409.

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RESULT 6
AAI92484/c
ID AAI924
XX AAI924
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XX O6-NOV
XX Human
XX Human;
KW Vaccin
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             W0200164835-A2
                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                            Homo sapiens.
                                                                                                                                            Human polynucleotide SEQ ID NO 12544.
                                                                                                                                                                             06-NOV-2001 (first entry)
                                                                                                                                                                                                                                   AAI92484 standard; cDNA; 442 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to Cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and treatment of cancer, leukaemia, nervous system disorders, arthritis and treitmammarion
                                                                                                                                                                                                                                                                                                                         133 GTT 131
                                                                                                                                                                                                                                                                                                                                                     592 ggt 594
                                                                                                                                                                                                                                                                                                                                                                Sequence 423 BP; 205 A; 43 C; 87 G; 88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            532 cttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctgg 591
                                                                                                                                                                                                                                                                                                                                                                                                                                              472 aagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctcttt 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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53.0%;
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                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                          Homo sapiens.
                                                                                                                           Human polynucleotide SEQ ID NO 5364.
                                                                                                                                                             06-NOV-2001 (first entry)
                                                                                                                                                                                                                         AAI85304 standard; cDNA; 404 BP
                                                                                                                                                                                                     AAI85304;
                                                                                                                                                                                                                                                                                                    199 TTTTTTTTTTTTTTTTTTTTTT 177
                                                                                                                                                                                                                                                                                                                                532 cttcttttgccctttcttagctt 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 442 BP; 175 A; 73 C; 104 G; 83 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to production of cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, haematopolesis regulating activiny hibbin activity and may be useful in the diagnosis and/or inflammation cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                        472 aagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctcttt 531
                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
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18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45.4; DB 22; Length 442; Pred. No. 0.0045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61; Indels
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18-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 5364; 1399pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acids and polypeptides, useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 404 BP; 205 A; 47 C; 82 G; 62 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                              AAI83979 standard; cDNA; 416 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412 ttttttattgtcacacagaaaaggaaactgccttgtctcccttccgggaattctctcttt 471
             Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
                                                             Human polynucleotide SEQ ID NO 4039
                                                                                                                                                                                                                                                                                                                                                                                                        472 aagactgtaagtcgctgcctgagtggtttcattttgttttgttttcttccccttctcttt 531
                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue growth factor; immunomodulatory; cancer;
                                                                                                 06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                            532 cttcttttgccctttcttagcttgcactcccatggtgatttctqcttggtctcctgctgg 591
                                                                                                                                                                                                                                                                                                                                                                            592 ggttggtg 599
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2000US-0577409.
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          leukaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopoiesis regulating activity, tissue growth factor activity, hammatopoiesis regulation activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or activity forms.
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18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 416 BP; 210 A; 44 C; 91 G; 66 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                  Human polynucleotide SEQ ID NO 9244.
                                                                                                                                                     AAI89184 standard; cDNA; 420 BP
                                                                                      06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 412 ttttttattgtcacacagaaaaggaaactgccttgtctcccttccgggaattctctcttt 471
Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
                                                                                                                                                                                                                                                                                                           472 aagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctcttt 531
                                                                                                                                                                                                                                                                                                                                                                            532 cttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtct 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                 AAS44777;
                                                   AAS44777 standard; DNA; 424 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 420 BP; 204 A; 73 C; 65 G; 75 T; 3 other;
                                                                                                                       223 TTTTTTTTTTATT 211
                                                                                                                                               592 ggttggtggtact 604
                                                                                                                                                                532 cttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctgg 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                      itp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to human polynucleotides (AAI79941-AAI93841) and encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-514838/56.
                                                                                                                                                                                                                                                                                                                                    97;
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Drmanac RT
(first entry)
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                           5.7%;
                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                       Score 41.2; DB:
Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 420;
                                                                                                                                                                                                                                                                                                                             96;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                         Gaps
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Qy

Query Match Best Local Similarity

5.7**%**; 57.6**%**;

Score 40.8; DB Pred. No. 0.093;

DB 22; Length 424;

Sequence 424 BP; 138 A; 60 C; 110 G; 110 T; 6 other:

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as multiple sclerosis, connective tissue disease, rheumatoid arthritis, diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system concretes such as Parkinson's disease, Alzheimer's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and controled disease, inflammatory disorders such as nephritis, Crohn's compared disease, inflammatory disorders such as nephritis, Crohn's compared disease. The sequences exhibit activity relating to angiogenesis, con culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, accidental damage or genetic cartilage, tendons and ligaments and in tissue repair and burn healing. Concerning the sequences may also be used for regeneration, but were obtained in electronic format directly from WIPO cat figure to but were obtained in electronic format directly from WIPO xxx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAS44576-AAS44919 represent full-length polynucleotides and contig polynucleotides encoding polypeptides of the invention. The DNA and protein sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as a human, dog, monkey, mouse, hamster or rat. The disorders include cancers such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 374; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in arrays for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-589862/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation; neurous system disorder; inflammatory disorder; cell differentiation; ds; angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair; cytostatic; antirheumatic; antiarthritic; vulnerary; antinflammatory; neuroprotective; osteopathic; antidabetic; antiparkinsonian; neuroprotective; osteopathic; antidabetic; antiasthmatic; antiallergic; immunostimulant; analgesic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAU27877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-2000;
14-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0515126.
2000US-0577409.
2000US-0597707.
2000US-0616807.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asundi V, Zhang J, Zhao Ç
T, Wang J, Ma Y, Wang D,
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n, Chen R,
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AAI81389/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 1449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI81389 standard; cDNA; 400 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI81389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 ttttattgtcacacagaaaaggaaactgccttgtctcccttccggggaattctctctttaa 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO19910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or reatment of cancer lenvesments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1449; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                 p-PSDB; AAO01458
                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTT 217
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sequence 400 BP; 184 A; 50 C; 85 G; 80 T; 1 other;

5.6%;

Score 40.6;

DB 22;

Length 400;

Sequence 410 BP; 197 A; 36 C; 119 G; 50 T; 8 other;

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RESULT 12
AAI89131/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polynucleotide SEQ ID NO 9191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-2001.
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                                                                                                              production of other cytckines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytckine-like activities, peptide therapy. The polypeptides have various cytckine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity individual activity and may be useful in the diagnosis and/or activity/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 9191; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immuno
                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                               treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                          2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                            AA009200
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                                                                                  The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and may be useful in the diagnosis and/or activity and activity activity and activity activity and activity activity activity.
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                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                        treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 12539; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001; 2001WO-US04927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI92479;
                ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   532 cttcttttgccctttcttagctt 554
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                                                                                                                                                                                                                                                                                                                                                                 2001-514838/56.
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                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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Sequence 410 BP; 170 A; 54 C; 107 G; 71 T; 8 other:

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AAZ17263/c
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one suspected of being cancerous, where the gene product is encoded by one polynucleotide sequences given in AAZ12532 to AAZ1779. The polynucleotides can be used as a source of primers and probes, which can mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides
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                                                                                                                                                                         Claim 1; Page 2250-2251; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-1998;
28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
                                                                                                                                                                                                    Novel human genes and their expression products differentially expressed in different cell types
                                                                                                                                                                                                                                                  WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                          Stache-Crain B, Sudduth-Klinger J,
                                                                                                                                                                                                                                                                                             Jones WL, Kassam A,
Lamson G, Leshkowit;
                                                                                                                                                                                                                                                                                                                                   Crkvenjakov R,
                                                                                                                                                                                                                                                                                                                    Escobedo J,
                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09938972-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene expression product cDNA sequence SEQ ID NO:4735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ17263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ17263 standard; cDNA; 1337 BP
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                                                                                                                                                                                                                                                            Dickson M, Drmanac , arcia PD, Garcia V, Giese K, Innis , sam A, Kennedy GC, Kita D, Labat I; hkowitz D, Pot D, Randazzo F, Reinh , knikowitz D, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                      98US-0080515
                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0075954
98US-0080114
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                                                                                                                                                                                                                    products which are
                                                                                                                                                                                                                                                                                                               Innis MA;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI88050 standard; cDNA; 398 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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   Claim 1; SEQ ID NO 8110; 1399pp + Sequence Listing; English
                                                                                                 Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                               WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                       P-PSDB; AAO08119.
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Similarity 38.4%;
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pred. No. 0.18;
0; Mismatches 146;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production and polypeptides are useful in gene therapy vaccines or polynucleotides and polypeptides have various cytokine-like activities, peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity. insue growth factor activity, immunomodulatory activity and treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 398 BP; 162 A; 72 C; 71 G; 81 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                    407 taccgttttttattgtcacacagaaaaggaaactgccttgtctcccttccggggaattctc 466
                                                                                                                          527 tetttettettttgecetttettagettgeacteceatggtgatttetgettggteteet 586
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207 GAGGGTTCTTCTACTATTAGGACTTTTCGCTTCGAAGCGAAGGCTTCTCA 158
                                     gctggggttggtggtactcgttcccaccgcacagaacccggcgcctatta 636
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Pred. No. 0.12;
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Search completed: September 7, 2002, 18:40:33 Job time: 29927 sec

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by |chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match Length DB
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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 /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-232-463-14
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US-08-232-463-14
US-08-26-678A-24
US-08-520-678A-24
US-09-268-992-7
US-09-268-992-7
US-09-288-59-564-1
US-09-39-964-1
US-09-256-490-1
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US-08-659-251-1
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PCT-US96-61445-14
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US-09-266-1490-1
PCT-US96-11445-14
US-08-659-251-7
US-09-268-1490-1
PCT-US96-11445-14
US-08-659-251-7
US-09-268-1449-1
US-09-268-1448-196-17
US-09-268-1448-366-7
US-08-680-366-7
US-08-680-366-7
US-08-09-018-584A-9
US-09-007-005-17
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US-08-232-463-14  US-08-232-463-14  US-08-232-463-14  Application US/08232463  Patent No. 5670367  GENERAL INFORMATION: APPLICANT: DORNER, F. G. APPLICANT: DORNER, F. G. APPLICANT: FALKNER, F. G. APPLICANT: SCHEIFLINGER, F. G. APPLICANT: SCOURNESS: CORRESPONDENCE ADDRESS: SOUTHVARE: SLOPEY ALIANT FOWLPOX VIRUS  NABDIUM TYPE: Floppy disk COMPUTER: 1800 Diagonal Road, Suite 500  STATE: VA. COUNTRY: USA COUNTRY: USA COMPUTER: IBM PC compatible OPERATING TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PCDS/MS-DOS SOFTWARE: PATENT FLORES #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/232,463 FILING DATE: APPLICATION NUMBER: US/08/232,463 FILING DATE: 26-AUG-1991 APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 APTORNAY/ACENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELECOMMUNICATION I	ALIGNMENTS	C 28 34.2 4.8 1635 3 US-09-234-332-4 C 29 34.2 4.8 5433 3 US-08-929-329-1 C 30 34.2 4.8 20303 1 US-08-370-9758-6 C 31 34.2 4.8 26764 1 US-08-370-9758-1 C 32 34 4.7 1431 6 5465783-1 C 33 34 4.7 1431 6 5465783-1 C 33 38 4.7 1798 2 US-09-105-537-21 C 35 33 8 4.7 1798 2 US-09-105-537-3 C 37 33.8 4.7 13613 4 US-09-105-537-3 C 39 33.8 4.7 1065 1 US-09-120-878-19 C 40 33.4 4.6 291 4 US-09-329-796-1 C 41 33.4 4.6 7208 4 US-09-323-923-107 C 43 33.2 4.6 1065 3 US-09-313-932-107 C 44 33.2 4.6 1065 5 PCT-US95-09377-1 C 44 33.2 4.6 1065 5 PCT-US95-09377-1
		Sequence 4, Appli Sequence 1, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 8, Appli Sequence 21, Appli Sequence 12, Appli Sequence 11, Appli Sequence 11, Appli Sequence 107, App Sequence 107, Appli Sequence 107, Appli Sequence 1, Appli

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US-08-232-463-14
                                                                                                                            ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)883-4109
TELEFAX: (703)683-4109
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                                                                           TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08232463 Patent No. 5670367
                         TOPOLOGY: line
IMMEDIATE SOURCE:
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Best Local :
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                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. APPLICANT: FEGURET,
                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                 CLONE:
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                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                  nucleic acid
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                                                     single
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26-AUG-1991
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8.2%; Pred. No. 7.6e-06;
ive 159; Mismatches 109; Indels
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US-08-162-809-1
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Best Local Similarity
""" trhes 8; Conserve
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                                                                                                           TELEFAX: (619) 535-89.
INFORMATION FOR SEQ ID NO:
                                  FEATURE:
                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 3133 base pairs
                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                        MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                           TOPOLOGY:
                                                          STRANDEDNESS:
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                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           STREET: 4370 La
CITY: San Diego
STATE: Californi
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                                                                                                                                                                                                                                                                                                                                                                                             4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasquale, Elena B.
Sajjadi, Fereydoun G.
Sajjadi, Fereydoun G.
WENTION: NOVEL EPH-RELATED TYROSINE KINASES,
WYENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
join(3..419, 421..2858)
                 CDS
                                                                                                                                                                                                                                                                                                                                                        United States of America
                                             linear
                                                                                                                                        (619)
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                                                          both
                                                                                                                          535-8949
                                                                                                                                        535-9001
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; MOLECULE TYPE:
US-08-520-678A-24
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Best Local :
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                                    Matches
                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                           NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3004 GGGACTCGCCTCGGCCTGGTGACTTCCATCCCTCAC 3039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2944 GCCGCAGCTGGAGAGGGGCAGCCACGGCCGGGGCTGTGCCTGACCGCGGAGGACGTTCCT 3003
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 accccggttggagagaggagcggaactcctggacaagccctgacaagccaagccaaaggt 189
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 257 base pairs
                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 314-727-5188
                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Henderson, melodie W.
REGISTRATION NUMBER: 37,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 ccgctccggcgcgggtgggtgagtgcgcgccccc 225
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STREET:
CITY: S
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/520,678A
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                                                    Local Similarity
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48.6%;
                                                    5.2%;
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                                                                                                                                                                                                                                                                                                                                  6029-6836
                                                    Score 37.8;
Pred. No. 0.
                                        Mismatches
                                                      0.083;
                                                                     DB 2; | Length 257;
                                        47; Indels
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Best Local Similarity
Thes 66; Conserve
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                                 US-09-268-992-7/c
                                                   RESULT
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Sequence 24, App
--+ No. 62970
Sequence 7, Application US/09268992 Patent No. 6342351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rice, Charles M.
APPLICANT: KOLYKhalov, Alexander A.
APPLICANT: KOLYKhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                          539 tgccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctgg 591
                                                                                                                                                                          CITY: St.
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                                                                                                       174 TTTTTTTCTTTCCTTCCTTTTTCCCTTTCTTTCTTCCTTCTTTAATGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
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7733 Forsyth Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                          257 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                  58.4%;
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                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                  Score 37.8; DB 4; Length 257; Pred. No. 0.083;
                                                                                                                                                                                                                                                     47;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                     Gaps
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GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
LEGGTH: 123
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                        ; OTHER INFORMATION: Translation template US-09-007-005-1
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: LCCATION: all n positions
: OTHER INFORMATION: n-a, c, g, or t
US-09-268-992-7
               Matches
                                 Best. Local
                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09007005B Patent No. 6258558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 7
LENGTH: 72604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 09/236,134
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: 60/106,056
EARLIER FILING DATE: 1998-10-28
EARLIER APPLICATION NUMBER: 60/088,312
EARLIER FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 60/078,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/268,992
CURRENT FILING DATE: 1999-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chen, H.
APPLICANT: Freimer, N.
APPLICANT: Freimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
FILE REFERENCE: 7853-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 tgccctttcttagcttgcactcccatggtgatttctgcttggtctcctgct 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y Match 5.2%;
Local Similarity 58.6%;
         5.2%; Score 37.2; DB Similarity 39.1%; Pred. No. 0.091; 36; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
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  29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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                                           DB 4; Length 123;
      27;
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Gaps
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0;
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(3988)
US-09-339-964-1
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FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER: FILING DATE: 1998-01-14
NUMBER: FILING DATE: 1998-01-14
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                                                                                                                             SEQ ID NO 1
LENGTH: 4743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
LENGTH: 123
                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/339,964
CURRENT FILING DATE: 1999-06-25
                                                                                                                                                                                                                                      APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-2 EXPRESSION
FILE REFERENCE: RTS-0065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                        NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
                                                                             ORGANISM: Homo sapiens
                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               558 ctcccatggtgatttctgcttggtctcctgct 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 YTYCYAYGYTYTYTYCYTYGYTYTCYCYAYT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 5.2%;
Local Similarity 39.1%;
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Pred. No. 0.091;
""" aratches 27;
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NAME/KEY: misc_feature

; LOCATION: (1)...(152331)

; OTHER INFORMATION: n = A,T,C or G

US-09-128-155-16
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APPLICANT: Pan, Yang
TITLE OF INVENTION: MOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
                                                                                                                                                  US-09-018-584A-13
                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 16, Application US/09128155 Patent No. 6117654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 16
                                                                                                             Sequence 13, Application US/09018584A Patent No. 6238863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
GENERAL INFORMATION:
APPLICANT: Schumm, James W.
APPLICANT: Bacher, Jeffery W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
TITLE OF INVENTION: REPEAT DNA MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4348 ttccaccgggcctgaaccacagcggaggagctccgctaagacctccccaccccccgctggg 4407
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                          ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 ggtgggcgtggggggggaagtggaattgaagcggaagtctgggaagc 109
                                                                                                                                                                                                                                                    125 gggggaccccggttggagagaggagcggaactcctggacaagccctgacaagccaagcca 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 tgggcgtgggggggggacaggaattgaagcggaagtctgggaagctttagggtcgctgga 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 ccgctgggcaggcgggcagctccggcgctcctcggagaccactgcgctccacgttgagg 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 152331;
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                                                                                                                                                                                                                                                                                               RESULT 12
US-08-659-251-14/c
                                                                                                                                                                                                                                               ; Patent No. 5883081 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                Sequence 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word 97 (DOS CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: G132
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
                                                                                                                                         APPLICANT: Talbott, Kanuy
APPLICANT: Poeschla, Eric
TITLE OF INVENTION: Isolation of No. 5883081el HIV-2 Proviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                              APPLICANT: Kraus, Guenter
APPLICANT: Wong-Staal, Fl
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   549 tagettgeacteceatggtgatttetgettggteteetget 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                          489 cctgagtggtttcattttgttttgtttttctgcccttctctttttcttttttctttttgccctttct 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Grady J. Fren
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              7 Match 4.9%; Score 35.4; DB 4; Length 372; Local Similarity 59.4%; Pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY:
                                                                                                                                                                                                                                                                                                                                                              CHROMOSOME/SEGMENT: 4 gter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                               COUNTRY: USA
ZIP: 94111-3834
                                                                STATE:
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G132
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Talbott, Randy
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US-09-256-490-14/c
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                                                                                                                                                                                                                                        Patent No. 6235881
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                     APPLICANT: Talbott, kanuy
APPLICANT: Poeschla, Eric
TITLE OF INVENTION: Isolation of No. 6235881el HIV-2 Proviruses
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                        APPLICANT: APPLICANT:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                            615 gcac 618
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OTHER INFORMATION:
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OTHER INFORMATION:
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REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 02307E-056410US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                     555 gcactcccatggtgatttctgcttggtctcctgtgtggggttggtggtactcgttcccacc 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 CTGTCACCTCCTTGTATGGTCTCATTTTCTGCTCTTTCTGCTTCCTCCCTTGCTGCAAGT 189
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FILING DATE: 26-JUL-1995
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3168 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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Talbott, Randy
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49.5%; Pred. No. 1.3;
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/note= "HIV-2KR subsequence encoding
pol gene"
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
                                                                                                                                                                                               APPLICANT: The Regen
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                     615 gcac 618
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LOCATION: 1..3168
COTHER INFORMATION:
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REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                               STREET: 201 N. Figueroa Street, CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 CTGTCACCTCCTTGTATGGTCTCATTTTCTGCTCTTCTGCTTCCTCCCTTGCTAGGT 189
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                                                                                           COUNTRY:
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                                                                                                                STATE:
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Local Similarity 49.5%;
es 91; Conservation
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: II
                                                                          90012-2628
                                                                                                            California
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                                                                                              USA
                                                                                                                                                                                                                The Regents of the University of California VENTION: Isolation of Novel HIV-2 Proviruse:
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/note= "HIV-2KR subsequence encoding
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Pred. No. 1.
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                                                                                                                                              5th Floor
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Berliner, Robert
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OTHER INFORMATION:
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OTHER INFORMATION:
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              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                    COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                       CITY: San Francisco
                                                                                                                                                                     STREET:
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                                                                                                                                   California
                                                                                                                                                                       Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                            Poeschla, Eric
VENTION: Isolation of No. 5883081el HIV-2 Proviruses
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49.5%; Pred. No. 1.3;
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/note= "HIV-2KR subsequence encoding
pol gene"
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 Mismatches

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                                                                                                                                                                                                                                                              Query Match 4.9%;
Best Local Similarity 49.5%;
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/001,441 FILING DATE: 26-JUL-1995 ATTORNEY/AGENT INFORMATION: NAME: GAITELT-Wackowski, Eugenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 10163 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                  2601 GCAAATCCTCTGTCGCCTCTTTGTGTGGTGTCTCCTTCTTCGAGGTGCAGTAAGTCCT 2542
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                           2481 ACTTCTCTAGCAGGTCTGCTGGGGGTCTGGTGGGGGGTGCTGTTGGTGTCAGCCCCTGCG 2422
                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
2421 GGAC 2418
                                                                                                                      615 gcac 618
                                                                           555 gcactcccatggtgatttctgcttggtctcctgctggtggtttggtggtactcgttcccacc 614
                                                                                                                                                 435 gaaactgccttgtctcccttccgggaattctctcttttaagactgtaagtcgctgcctgag 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: No. 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                  91;
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                             1..10163
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                                                                                                                                                                                                                                                                                                                                            /note= "HIV-2KR provirus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/659,251
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                                                                                                                                                                                                                                                                  Score 35.2;
Pred. No. 2;
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                                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                                                                   Length 10163;
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0; Gaps

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Search completed: September Job time: 28877 sec 7, 2002, 18:23:03

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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2: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*

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(Cgn2_6/ptodata/2/pna/US096C_COMB.seq:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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166.4			٠	•	•	173.8	7	178.8	•	179.6			182.6			186.4		188.4	190.2	190.2	203.4	203.4	203.4	262.8	296.8	611.8	611.8	713	716.8	720	Score
													25.4			25.9													9	100.0	Query Match I
263	263	2760	2760	2760	2760	2760	1368	462	453	564	443	473	473	473	473	362	362	532	466	466	575	419	419	266	467	2827	2380	3212	45121	720	Length [
40	12	25	25	25	25	25	71	28	29	20	19	34	34	16	16	23	19	29	<u>u</u>	17	18	35	18	32	56	32	32	32	36	32	DB .
018-911-	US-08-869-540-581	-09-652-91	-09-652-81	-652-12	-09-652-12	-09-644-8	-60-324-18	-716-47	-726-78	-534-84	9-522	564	9-904	US-09-248-797-39624	611 - 387	-081-898	US-09-522-303-847		9-817-500	-909	9-	-943-143	-09-489-036-		-360-3	-09-834-29	US-09-834-291-3	-09-	-09-997-72	US-09-834-291-2	ID
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Sequence 2, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
PLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
                                                                                                                                                                                                                                                                                                                ; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-2
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PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                          61
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                                                                                                                                                                                                                                 1 gatcccgctgggcaggcggggcagctcctcgggcgctcctcggagaccactgcgctccacgtt 60
                                 gagcctacagccttcagaacacatattgctcattttctggcagttctcagacgtaggaaa
      ctcgaaaaagttatatgggggctgaatgagcttctggaggcttgtttaccgttttttatt
                                                                                gagcctacagccttcagaacacatattgctcattttctggcagtttctcagacgtaggaaa
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                                                                                                                                                                                                                                                                720;
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 720; DB 32; 100.0%; Pred. No. 2.4e-152; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-362-510-3927

US-09-362-510A-3927

US-09-904-013-3927

US-60-172-373-10224

US-09-652-127-2780

US-09-652-127-2780

US-09-652-111-10283

US-09-652-911-10283

US-09-396-087-4122

US-09-396-087-4129

US-09-431-517-12154
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12154, A
24990, A
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7725, A
10283,
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3927, Ap
10224, Ap
10224, Ap
2780, Ap
2780, Ap
1725, Ap
10283, A
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US-09-997-722-10
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PRIOR FILING DATE: 2000-12-22
PRIOR PPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 45121
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Best Local
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APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
                                                                                                                                                                                                                                                      10494 gatcccgctgggcaggcggggcagctccgggggtcctcgggagaccactgcgctccacgtt 10553
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ORGANISM: Homo sapiens
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gccaaaggtccgctccggcgcgggtgggtgagtgcgccccgcccccgcggggggcgggggaga 240
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Pred. No. 3.2e-151;
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CURRENT EILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE9/03343
PRIOR FILLING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILLING DATE: 1998-10-16
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2740 gagcctacagccttcagaacacatattgctcattttctggcagttctcagacgtaggaaa
                241 gagcctacagccttcagaacacatattgctcattttctggcagttctcagacgtaggaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122 CURRENT APPLICATION NUMBER: US/09/834,291 CURRENT FILING DATE: 2001-08-21 PRIOR APPLICATION NUMBER: PCT/DE99/0343 PRIOR FILING DATE: 1999-10-18 PRIOR APPLICATION NUMBER: DE 198 47 779.1 PRIOR FILING DATE: 1998-10-16
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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1946 ctcagacgtaggaaataagtcagcaccgaagcagtggttaagccggagggctcggaagaa 2005
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99.7%;
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Pred. No. 8.8e-128;
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SEQ ID NO 4
LENGTH: 2827
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APPLICANT: Krammer, Peter
APPLICANT: Krammer, Peter
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09834291
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/834,291 CURRENT FILING DATE: 2001-08-21 PRIOR APPLICATION NUMBER: PCT/DE99/03343 PRIOR FILING DATE: 1999-10-18 PRIOR APPLICATION NUMBER: DE 198 47 779.1 PRIOR FILING DATE: 1998-10-16 NUMBER OF SEQ ID NOS: 32
                                                                         2333
             2393
                                                                                                                                                                                      2213 aagctttagggtcgctggagggggaccccggttggagagaggagcggaactcctggacaa 2272
                286 ctcagacgtaggaaataagtcagcaccgaagcagtggttaagccggagggctcggaagaa 345
                                                                                                                                                                                                      106 aagetttagggtegetggaggggaeeeeggttggagagggageggaaeteetggaeea 165
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ctcagacgtaggaaataagtcagcaccgaagcagtggttaagccggagggctcggaagaa
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                                                                             909999909999agagagoctacagocttcagaacacatattgotcattttctggcagtt 285
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Pred. No. 9.2e-128;
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; OTHER INFORMATION: Incyte ID No: 038693.2c
US-60-172-360-3705
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APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
FILE REFERENCE: GX-0007 P
CURRENT APPLICATION NUMBER: US/60/172,360
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 29838
SOTTWARE: PERL Program
SEQ ID NO 3705
LENGTH: 467
TYPE: NO. 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                      601 tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct
                                                                            541 ccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctggggttggtgg
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99.3%;
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Pred. No. 9.1e-57;
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; LENGTH: 266
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-32
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-489-036-818
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                                                                                                                                                                                                                             Sequence 818, Applicating GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
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Best Local Similarity
                                                    CURRENT APPLICATION NUMBER: US/09/489,036
CURRENT FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 35324
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 818
LENGTH: 419
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PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                     TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From Various Libraries FILE REFERENCE: 783
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Pred. No. 3.9e-49;
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PRIOR APPLICATION UNMBER: 09/489,036
PRIOR FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 35324
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 818
LENGTH: 419
TYPE: DNA
ORGANISM: Homo sapiens
US-09-943-143-818
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US-09-471-275-3315/c
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/943,143
CURRENT FILING DATE: 2001-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 gaccccgctgggcaggcgggcagctccgggggctcctcggagaccactgcgctccacgtt 166
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Sequence 3315, Application US/09471275
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 782

CURRENT APPLICATION NUMBER: US/09/471,275

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RESULT 11
US-09-333-909-2214
; Sequence 2214, Application US/09333909
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; NAME/KEY: misc_feature
; LOCATION: (465)...(578)
; OTHER INFORMATION: similar to gi178067 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-471-275-3315
          APPLICANT: Gearing, David P.
APPLICANT: Pan, Yang
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED
TITLE OF INVENTION: HUMAN OSTEOBLAST LIBRARY
FILE REFERENCE: MLN98-29pM
CURRENT APPLICATION NUMBER: US/09/333,909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 10451
SOFTWARE: pt_CT_genes Versi
SEQ ID NO 3315
LENGTH: 575
CURRENT FILING DATE: 1999-06-16
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EARLIER
EARLIER
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EARLIER APPLICATION NUMBER: US 09/277,227
EARLIER FILING DATE: 1999-03-25
EARLIER APPLICATION NUMBER: US 09/271,490
EARLIER FILING DATE: 1999-03-18
EARLIER FILING DATE: 1999-03-18
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                       181 gccaaaggtccgctccggcgcgggt 205
                                                                                                                                                                                                                                                                                                                                                              121 tggagggggaccccggttggagagagggagctcctggaccaggccttgaccagccaa 180
                                                                                                                                                                                                                                                                                                                                                                                                                        253 GAGGTGGGCGTGGGGGGGGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 GACCCCGCTGGGCAGGCGGGCAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                61 gaggtgggggtggggggggacaggaattgaagcggaagtctggggaagtcttagggtcgc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 gatcccgctgggcaggcggggcagctcctcggcgctcctcggagaccactgcgctccacgtt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                  GCCAAAGGTCCGCTCCGGCGCGGGT 109
                                                                                                                                                                                                                                                                                                                                             TGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACTCCTGGACAAGCCCTGACAAGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/399,720
FILING DATE: 1999-09-21
APPLICATION NUMBER: US 09/404,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/126,605
FILING DATE: 1999-03-26
APPLICATION NUMBER: US 09/306,350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1999-09-21 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1999-03-23
APPLICATION NUMBER: US 60/125,453
FILING DATE: 1999-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/293,972 FILING DATE: 1999-04-15 APPLICATION NUMBER: US 09/274,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/234,611
FILING DATE: 1999-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/240,371 FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/235,076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1999-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 575;
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288 cagacgtaggaaataagtcagcaccgaagcagtggttaagccggagggctcggaagaacg 347

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TYPE: DNA

ORGANISM: Homo sapiens
FEAGUTE:
NAME/KEY: misc_feature
LOCATION: (1)...(466)
OTHER INFORMATION: n = A,T,C or G
US-09-817-500-2214
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/817,500
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/089,519
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: US 60/135,628
PRIOR FILING DATE: 1999-05-24
PRIOR APPLICATION NUMBER: US 09/333,909
PRIOR FILING DATE: 1999-06-16
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 2409
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US-09-817-500-2214
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             Matches
                               Query Match
Best Local
                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Pan, Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2214, Application US/09817500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM TITLE OF INVENTION: HUMAN OSTEOBLAST LIBRARY FILE REFERENCE: 1600.1029-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/089,519
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/135,628
EARLIER FILING DATE: 1999-05-24
NUMBER OF SEO ID NOS: 2409
                                                                                                                                                                                                                                                               LENGTH: 466
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LOCATION: (1)...(466)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 466
        Local Similarity hes 207; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 ctttaagactgttcttacgtctgttgctagattatcgtccaaaagtgttaatgccc 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 ctttaagactgtaagtcgctgagtggtttcattttgtttttgtttttctgccc 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 accgttttttattgtcacacagaaaaggaaactgccttgtctcccttccgggaattctct 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 cagacgtaggaaataagtcagcagcagcagtggttaagccggagggctcggaagaacg 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 cggacgtaggaaataagtcngcaccgaagcagtggttaagccggagggctcggaagaacg 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcaccttttcttctcgaaaaagttatatgggggctgaatgagcttctggaggcttgttt 407
        Conservative
                          26.4%;
87.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.4%;
87.7%;
Score 190.2; DB 31; Length 466; Pred. No. 1.1e-32; 0; Mismatches 29; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 190.2; DB 17;
Pred. No. 1.1e-32;
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    0;
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Gaps
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  0;
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GENERAL INFORMATION:

APPLICANT: Gearing, David P.

APPLICANT: Gearing, Douglas A.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM

TITLE OF INVENTION: HUMAN WAMMARY EPITHELIUM LIBRARY

FILE REFERENCE: 1600. 1086-001

CURRENT APPLICATION NUMBER: US/09/522,303

CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: 65/123,393

EARLIER FILING DATE: 1999-03-08

LEARLIER FILING DATE: 1999-03-08

LEARLIER FILING DATE: 1999-03-08
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 7691
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 5938
LENGTH: 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kingsbury, Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2051-001
CURRENT APPLICATION NUMBER: US/09/726,788
CURRENT FILING DATE: 2000-11-30
CURRENT FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gearing, David P. APPLICANT: Kingsbury, Gilli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/168,131 PRIOR FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                      346
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                                                                                                                                                                                                                                                                                                                                 466 ctctttaagactgtaagtcgctgcctgagtggtttcattttgtttttgtttttctgccc 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
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                                                                                                                                                                                                                                                                                                             193 ctctttaagactgttcttacgtctgttgctagattatcgtccaaaagtgttaatgccc 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 cccgcacgtcggaaataagtcagcaccgaagcagtggttaagccggagggctcggaagaa 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctttaagactgttcttacgtctgttgctagattatcgtccaaaagtgttaatgccc 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctttaagactgtaagtcgctgcctgagtggtttcattttgtttttgtttttctgccc 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              accgttttttattgtcacacagaaaaggaaactgccttgtctcccttccgggaattctct 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  accgttttttattgtcacacagaaaaggaaactgccttgtctccccttcccgggaattctct 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cggcaccttttctttctcgaaaaagttatatgggggctgaatgagcttctggaggcttgt 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cggcaccttttcttctcgaaaaagttatatgggggctgaatgagcttctggaggcttgt 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 29; Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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; LENGTH: 362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-522-303-847
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/14:
PRIOR FILLING DATE: 1999-07-14
NUMBER OF SEQ ID NOS: 2240
SOFTWARE: FastSEQ for Windows V.
SEQ ID NO 898
LENGTH: 362
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HOltzman, DUNYALL APPLICANT: HOLTZMAN, DAVID P.
APPLICANT: Gearing, David P.
TITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM LIBRARY
TITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM LIBRARY
TITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM LIBRARY
TITLE REFERENCE: 1600.1146-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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CURRENT FILING DATE: 2000-07-14
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                                                                                                                                      113 gggtgcggacaggaattgaagcggaagtctgggaagctttagggtcgctggagggggacc
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ctccggcgcgggtgggttcttacg
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Pred. No. 7.5e-32;
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Search completed: September 7, 2002, 22:32:03 Job time: 43817 sec

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pna/U

2: /cgn2_6/ptodata/2/pna/U

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Listing first 45 summaries
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/cgn2_6/ptodata/2/pna/US06_NEW_COMB. seq: *
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/cgn2_6/ptodata/2/pna/US08_NEW_COMB. seq: *
/cgn2_6/ptodata/2/pna/US09_NEW_COMB. seq: *
/cgn2_6/ptodata/2/pna/US10_NEW_COMB. seq: *
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S US-10-155-881-6250

S US-10-027-632-104181

S US-10-027-632-174395

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S US-10-027-632-325093

S US-10-103-313-632

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S US-10-037-632-11879

S US-10-035-832-971

S US-10-035-832-971

S US-10-176-912-202

S US-10-176-912-202

S US-10-184-634-202

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S US-10-037-632-33988

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S US-10-038-754-6470
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  Sequence 1262, Ap
Sequence 8585, Ap
Sequence 8585, Ap
Sequence 6250, Ap
Sequence 2987, Ap
Sequence 104181,
Sequence 114395,
Sequence 114395,
Sequence 325093,
Sequence 561, App
Sequence 561, App
Sequence 971, App
Sequence 971, App
Sequence 971, App
Sequence 272, Appl
Sequence 202, Appl
Sequence 203, Appl
Sequence 203, Appl
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Sequence 209, Appl
Sequence 209, Appl
Sequence 393, Appl
Sequence 992, Appl
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y 99 rvativ [1]     [1]    gggggc [1]     gggggc [1]   [1]   [1]	Dation David Ard, Eri ROYEL L249/RM NUMBER: 2000-12 2000-12 2001-03 S: 1613 version	346 1171 1480 610 610 776 777 18951 14951 24048 353 656 656 656 656 656 656 656 656 656
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RESULT 3
US-10-198-846-8585
; Sequence 8565, Application US/10198846
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 1276
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SEO ID NO 123
LENGTH: 710
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local
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                  APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhe
     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PM006C1N
CURRENT APPLICATION NUMBER: US/10/222,927
CURRENT FILING DATE: 2002-08-19
CURRENT FILING DATE: 2007-758 466
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Steinmann, Kathleen
              Xu, Yongyao
Wang, Youzhen
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                                                                                                                                                                                                                                                                                                                                          US-10-198-846-8585
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: THERAPY OF BREAST CANCER CURRENT EPILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR APPLICATION NUMBER: 60/306,220

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 8585

LENGTH: 931

THERE OF SEQ ID NOS: 14084

SEQ ID NO 8585
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 541, 542, 544, 550, 554,
LOCATION: 607, 629, 638, 658, 660,
LOCATION: 718, 724, 726, 728, 728,
LOCATION: 770, 773, 779, 780, 792,
LOCATION: 770, 773, 779, 780, 792,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: 229, 231, 234, 256, 294, 295, 299, 309,
LOCATION: 339, 344, 357, 360, 361, 363, 366, 369,
LOCATION: 412, 418, 424, 426, 428, 432, 437, 441,
LOCATION: 462, 463, 470, 471, 472, 478, 503, 506,
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 832, 833, 843, 845, 854,
LOCATION: 909, 929, 930
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
897 ng 898
                                                    238 ag 239
                                                                                                                    777 ggnnggggggggatgngaggatgnngggggggggagaagagaggangnnnaaggannagg
                                                                                                                                                                                                                                                     Local Similarity 44.5%; ses 81; Conservation
                                                                                                                                             cyctggagggggaccccggttggagagagggagctcctggacaagccctgacaagc 177
                                                                                                                                                                                                          9ttgaggtgggcgtggggcggacaggaattgaagcggaagtctgggaagctttagggt 117
                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                     Score 40.8; Di
Pred. No. 3.1;
                                                                                                                                                                                                                                                     Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                , 555, 557,
, 663, 666,
, 735, 746,
, 800, 801,
                                                                                                                                                                                                                                                                                                                                                                                    868,
                                                                                                                                                                                                                                                                                                                                                                                    872,
                                                                                                                                                                                                                                                                                    DB 6; Length 931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                561,
675,
749,
822,
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701,
754,
824,
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380,
444,
520,
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, 703, 710,
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, 825, 826
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387, 397,
456, 459,
528, 538
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407,
460,
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                                                                                                                         836
                                                                                                                                                                                                                                                    0;
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: Sequence 7588, Application US/10098754 : GENERAL INFORMATION:

APPLICANT: Harrington, John J APPLICANT: Jackson, P. David

APPLICANT:

Sherf, Bruce Cain, Scott Rundlett, St

Bruce A. Stephen

APPLICANT:

US-10-098-754-7588/c

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NAME/KEY: misc_feature
; LOCATION: (1)...(1021)
; OTHER INFORMATION: n = A,T,C or G
US-10-098-754-7588
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7588
LENGTH: 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                             SEQ ID NO 6250
LENGTH: 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 09/791539
PRIOR FILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ramachandran, Rakesh
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
FILE REFERENCE: ATX-001CN
CURRENT APPLICATION NUMBER: US/10/098,754
CURRENT FILING DATE: 2002-03-15
                                                                         Query Match 5.7%;
Best Local Similarity 52.3%;
                                                          Matches
                                                                                                                                                                                                                                                                    APPLICANT: Lutfiyya, Linda L.

APPLICANT: McIninch, James
TITLE OF INVENTION: UUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
FILE REFERENCE: 38-21(15300)J
CURRENT APPLICATION NUMBER: US/10/155,881
CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dotson, Stanton B. APPLICANT: Kovalic, David K. APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 37595
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                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 accccggttggagagaggagcggaactcctggacaagccctgacaagccaagccaaaggt 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 GCGCNCGCGAGGGCCCCCGGCGCGCGCGCCCCGCAGGGCGCGGNCGCCCG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 ttttttattgtcacacagaaaaggaaactgccttgtctccctttccggggaattctctcttt 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 gccttcag 257
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Local Similarity 47.2%;
nes 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gggcaggcgggagcactccggcgctcctcggagaccactgcgctccacgttgaggtgggc 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 131; |Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40.8; DB 6; Pred. No. 3.2;
                                                            0; Mismatches
                                                                             Score 40.8; DB 7; pred. No. 3.9;
                                                          82; | Indels
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               US-10-027-632-104181/c

Sequence 104181, Application US/10027632

SEQUENCE INFORMATION:

APPLICANT: Wang, David G:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR PILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; Cea mays; ORGANISM: Zea mays; US-10-155-881-2987
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SEQ ID NO 2987
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FILE REFERENCE: 38-21(15300)J
CURRENT APPLICATION NUMBER: US/10/155,881
CURRENT FILING DATE: 2002-05-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
PRIOR APPLICATION NUMBER: US 60/193,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1964 TATTTTTGTGGGCCCCTAAAAAAAACATTTTCTTTTTCACGCCCCGGGGAAAAAAACTTT 1905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532 cttcttttgccctttcttagcttgcactcccatggtgatttctgcttggtct
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                                                                                                                                                                                                                                                                                                                                                                1140 GTCCGGCATGTTT 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1200 TTTTTTTTTTTTTTTTTACACAGAACAGATACAAATACATAGACAAGCAAAGCAACTA 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       592 ggttggtggtactcgttcccaccgcacagaacccggcgcctattattggccaagaaactt 651
                                                                                                                                                                                                                                                                                                                                                                                                        652 gagcagcctgttt 664
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McIninch, James
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47.4%; Pred. No. 5.1;
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                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PRIOR PRICATION NUMBER: US 60/198,676
PRIOR PRICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PRICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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                                                 Query Match
Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 174395
LENGTH: 787
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Sequence 174395, Application US/10027632
GENERAL INFORMATION:
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LENGTH: 787
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Best Local Similarity 55.6%;
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                  TYPE: DNA
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
424 acacagaaaaggaaactgccttgtctcccttccgggaattctctctttaagactgtaagt 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 acacagaaaaggaaactgccttgtctcccttccgggaattctctcttttaagactgtaagt 483
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                                                     Conservative
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55.6%;
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                                                               Score 40; DB 7; Length 787; Pred, No. 4.7;
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                                                 Mismatches
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US-10-027-632-174396
                                                           Sequence 32503, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 2000-07-12
PRIOR PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
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LENGTH: 787
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Best Local :
                     CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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PRIOR APPLICATION NUMBER: US 60/218,006
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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; ORGANISM: Human
US-10-027-632-325093
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 325993
LENGTH: 787
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SEQ ID NO 632
LENGTH: 6573
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CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
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4012 gtttttcgatgtgctgctggattcaatttgccagtattttattgaggatttttgcatcaa 407
                                                                          3952 attgatttgcatatgctgaaccagccttgcattcctagggatgaagccaacttgatcatg 4011
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OR APPLICATION NUMBER: US 60/198,676
OR FILING DATE: 2000-04-20
OR APPLICATION NUMBER: US 60/193,483
OR FILING DATE: 2000-03-29
OR APPLICATION NUMBER: US 60/185,218
OR APPLICATION NUMBER: US 60/185,218
OR FILING DATE: 2000-02-24
OR APPLICATION NUMBER: US 60/167,363
OR FILING DATE: 1999-11-23
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Local Similarity 55.6%;
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                                   Match 5.6%;
Local Similarity 47.9%;
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Pred. No. 8;
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-10-125-540-561
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Best Local Similarity 47.9%;
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Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 375
LENGTH: 6573
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CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214C1
                                                                   Query Match 5.6%;
Best Local Similarity 47.9%;
Matches 115; Conservative
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358 tttctcgaaaaagttatatgggggctgaatgagcttctggaggcttgtttttt 417
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Pred. No.
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                                                                        Mismatches 125;
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Sequence 971, Application US/10035832
GENERAL INFORMATION:
APPLICANT: MODITIS, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DOFP
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
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Best Local Similarity
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR ETILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR ETLING DATE: 1999-09-28
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,576
PRIOR ETILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: PatentIn version 3.1
SEQ ID NO 971
LENGTH: 30828
27592 tototgtgtagccctggctgacctggcactcactttgt 27629
                                                                        PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (30603)..(30828)
OTHER INFORMATION: "n" at positions 30603 thru 30828 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (22853)..(22872)
OTHER_INFORMATION: "n" at positions 22853 thru 22872 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (15334)..(15753)
OTHER INFORMATION: "n" at positions 15334 thru 15753 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(42) OTHER INFORMATION: "n" at positions 1 thru 42 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                      530 ttcttcttttgccctttcttagcttgcactcccatggt 567
                                                                                              470 ttaagactgtaagtcgctgcctgagtggtttcattttgttttgtttttctgcccttctct 529
                                                                                                                                                                                    410 cgttttttattgtcacacagaaaaggaaactgccttgtctcccttccgggaattctctct 469
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Pred. No. 15;
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Search completed: September 8, 2002, 01:10:14 Job time: 37092 sec

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	H80544 Yt04f01.51 H80544 Yt04f01.51 R85827 Y922g10.51 AL540709 AL540709 AV715411 AV715411 H1838027 603083875	36.0 398 10 H861 35.3 297 9 AA018 5 35.2 381 10 H865 7 27.4 419 10 R858 7 26.4 899 9 AL54 0 26.4 899 9 AV711 0 27.5 020 10 BT88	9 10 11 12 13
	AA058563 z155b04.s AA05856275 zf53903.s AA011028 ze34d02.s AA047220 zf49e11.s AA047220 zf49e11.s AA057418 zf59h03.s AA0520992 ze65f07.s H84298 ys95e09.s1	41.4 60 40.9 57 39.8 44 39.8 54 39.6 44 39.6 44 39.6 44 37.5 37	8765488
	Description BI763679 603049567	Query Match Length DB 74.6 793 10	:
		SUMMARIES 8	
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<u> </u>		)B seq length: 0 )B seq length: 2000000000	Minimum DB Maximum DB
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		13736207 seqs, 6748477542 residues	Searched:
		table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Scoring ta
	atcaaagagacgtg 720	US-09-834-291-2   120	Title: Perfect so Sequence:
	time 8462.63 Seconds alignments) Million cell updates/sec	September 7, 2002, 14:51:28; Search (without 1148.320	Run on:
		c - nucleic search, using sw model	OM nucleic
	Ltd.	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen L	

AG058793 BF248086 AL107031

ALIGNMENTS

## VERSION KEYWORDS RESULT 1 BI763679/c COMMENT REFERENCE SOURCE ORGANISM DEFINITION ACCESSION FEATURES Snoor AUTHORS TITLE JOURNAL source Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11474 row: e column: 17 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 793) 1 (bases 1 to 793) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) mRNA sequence. BI763679 BI763679.1 GI:15755257 B1763679 793 bp mRNA linear EST 25-SEP-2001 603049567F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5189752 5', High quality sequence stop: 7 /note-"Organ: pooled colon, kidney, stomach; Vector: /note-"Organ: pooled colon, kidney, stomach; Vector: pcMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is /organism="Homo sapiens" /db\_xref="taxon:9606" /clone="IMAGE:5189752" /clone\_lib="NIH\_MGC\_116" /lab\_host="DH10B" 786.

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                  AAUJSD53 603 bp mRNA linear EST zf55b04.s1 Soares retina N2b4HR Homo sapiens cDNA clone TMAGE.380815 3', mRNA sequence.
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Similarity 98.9%;
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Pred. No. 2.6e-89;
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                                                                                                    601 tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct 660
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                                                                                                                                                             TACTCGTTCCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCT
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577 bp
zf53903.sl Soares retina N2b4HR
IMAGE:380692 3', mRNA sequence.
AA056275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE Consortium (info@image.linl.gov) for Insert Length: 921 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501,
Tel: 314 286 1800
Fax: 314 286 1810
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/dev_stage="55 year old"
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/clone="IMAGE:380815"
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99.78;
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241 GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCANAGAGACGTG 300

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                                                                                                                                                                                                                                                                                                                                                                                                          541 ccctttcttagcttgcactcccatggtgatttctgcttggtctcctgctggggttggtgg 600
661 gttttgaaaagtccctcgctcagaaatgccagcttgcagatgg¢taatcaaagagacgtg 720
                                                                                                              181 TACTCGTTCCCACCGCACAGAACCCGGNGCCTATTATTGGCCAAGAACTTGAGCAGCCT 240
                                                                                                                                                         601 tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct 660
                                                                                                                                                                                                                                                                    121 CCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGG
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1. (bases 1 to 577)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 178.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 286 1800
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/lab_host="DH10B (ampicillin resistant)"
/lab_host="D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. " | 10 thers
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98.3%;
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421 gtcacacagaaaaggaaactgccttgtctcccttccgggaattctctctttaagact-gt 479
                                                                                          1 GTCNCACAGAAAAAGAAACTGCCTTGTCTCCCTTCCGGGAATTCTCTCTTTAAGACTNGT 60
                                                                                                                                                                                                        Local Similarity
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman Hillier, L., Clark, N., Dubuque, T., Le, M., Lennon, G., Marra, M., Parsons, J., M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                      double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pm773 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted for a feer their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "

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/db_xref="GDB:1277412"
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/clone="IMAGE:360867"
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                                                                                                                                                                                                        39.8%; Score 286.4; DB 9; Length 442; 99.0%; Pred. No. 3.5e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Glsh, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags. Generation and analysis of 280,000 human expressed sequence tags.
                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
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quality sequence stop: 471.
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAAGATGGCTAATCAAAGAGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661 gttttgaaaagtccctcgctcagaaatgccagcttgc-agatggctaatcaaagagacgt 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 tactcgttcccaccgcacagaacccggcgcctattattggccaagaaacttgagcagcct 660
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                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 447)

Hillier_L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU5/418 447 bp mRNA linear EST
zf59h03.s1 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:381269 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                        quality sequence stop: 339.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 a
/dev_stage="55 year old"
//lab_stage="55 year old"
//lab_nost="DH10B (amplicillin resistant)"
//note="Organ: eye; Vector; pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
                                                                                         /tissue_type="retina"
/dev_stage="55 year c
                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:381269"
                                                                                                                                   /sex="male"
                                                                                                                                                /clone_lib="Soares retina N2b4HR"
                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="GDB:1289526"
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99.3%;
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Pred. No. 3.4e-43;
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467 bp mRNA (linear EST 30-JAN-19)
ze65f07.sl Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:363877 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins Chissoe, S., Wardis, T., Lacy, M., Le, M., Mardis, E., Moore, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, M.B., Marcis, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                                              Genome Res. 6 (9),
97044478
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA020992.1 GI:1484745
                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                          Contact: Wilson RK
This clone is available royalty-free through LLNL; contact the
                                                                                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                    Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                     (bases 1 to 467)
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                        est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soares and M.Fatima Bonaldo. 109 \text{ c} 107 \text{ g} 133 \text{ t}
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Pred. No. 5.3e-43;
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                                                                                               ORGANISM
                                 AUTHORS
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High quality sequence stop: 265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 833 Std Error: 0.00
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 376)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., M., Hultman, M., Kucaba, T., Le, M., Tan, F., Trevaskis, E., Waterston Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
                                                                                                                                                                         ys95e09.sl Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222568 3', mRNA sequence.
                                                                                                                                                                                                            H84298
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111 c 119 g 122 t 10 others
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/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
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/clone="IMAGE:363877"
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                                                                                                                                                                                                                376 bp
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                                                                                             691 agcttgcagatggctaatcaaagagacgtg 720
                                                                                  241 AGCTTGCAGATGGCTAATCAAAGAGACGTG 270
                                                                                                                         181 CTATTATTGGCCAAGAAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCC
                                                                                                                                     631 ctattattggccaagaaacttgagcagcctgttttgaaaagtccctcggctcagaaatgcc 690
                                                                                                                                                                     121 TTCTGCTTGGTCTCCTGGTGGTTGGTGGTACTCGTTCCCACCGCACAGAACCCGGCGC 180
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nes 270; Conserv
            ys94g08.s1 Soares retina N2b5HR Homo sapiens cDNA clone
                                 H86126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
High quality_sequence stops: 364
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Contact: Wilson RK
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/dev_stage="55 year old"
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/clone="IMAGE:222568"
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/sex="male"
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/db_xref="GDB:3851329"
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High quality sequence stops: 378
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (Info@image.llnl.gov) for further information.
Insert Length: 925 std Error: 0.00
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The WashU-Merck EST Project
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/db_xref="GDB:3851255"
/db_xref="taxon:9606"
/clone="IMAGE:222494"
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297 bp mRNA linear EST ze50a08.sl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:362390 3', mRNA sequence.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq.primer: -40M13 fwd. from Amersham
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/clone="IMAGE:362390"
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                                                                                                                                                              99.6%;
                                                                                                                                   0;
                                                                                                                            Score 254.4; DB 9; Length 297; Pred. No. 2.9e-37; Indels 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l (bases 1 to 381)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yt04f01.sl Soares retina N2b5HR Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 882 Std E
Seq primer: Promega -21m13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 882 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
High quality sequence stops: 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE:223321 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Source: IMAGE Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
/organism="Homo sapiens"
/db_xref="GDB:3854355"
/db_xref="taxon:9606"
/clone="IMAGE:223321"
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                         /clone_lib="Soares retina N2b5HR"
                                                                                                                                                                                                                                                                     /tissue_type="retina"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ctattattggccaagaaacttgagcagcctgttttgaaaagtccctcgctcagaaatgcc 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTTGCAGATGGGCTAATCAAAGGAGG 268
                                                                                                                                                                           Email: est@watson.wustl.edu
Insert Size: 958
High quality sequence stops: 269
                                                                                                                                                                                                                                                                                                                                                                             Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 419)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston The WashU-Merck ES; Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259;
                                                                                                                                                                  High quality sequence stop: 269
                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        volution 419 bp mRNA linear EST yq22g10.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:274746 3', mRNA sequence.
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314 286 1810
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/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
                                                             /clone_lib="Soares retina N2b4HR'
                                                                              /db_xref="taxon:9606"
/clone="IMAGE:274746"
                                                  /sex="male"
                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:3798432"
                                                                                                                                                    ocation/Qualifiers
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96.6%;
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AUTHORS
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AL540709/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        643 aagaaacttgagcagcctgttttgaaaagtccctcgctcagaaatgccagcttgcagatg 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583 tcctgctggggttggtggtactcgttcccaccgcacagaacccggcgccctattattggcc 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GCTAATCAAAGAGACGTG 198
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                                                                                                                                                                                                                                                                                                                                          Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                        Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL540709 LTI_FL002_PL1 Homo sapiens
                                                                                                                                                                                                                                                                    Email: segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 899)
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                                                 Onte-Torgan: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life
pcMvSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                              /clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                 /clone="CS0DE002YN18"
                                                                                                                                                                                                                                                     Location/Qualifiers
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99.5%;
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Pred No. 9.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 GATCCCGCTGGGCAGGCGGGCAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTT 131
294 taggamatamagtcmgcaccgmagcagtggttmagccggmagggctcggmagamacggcacct 353
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                                                                                                                                                                                                                                                                                                                                                                                         Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
S51 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801912(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y!, Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                                                                                                                                                                                                            Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,G., Cheng,Z. and Han,Z.
Homo sapiens cDNA DCB clones
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                                                                                                                                                             /note="Vector: pTriplEx2; Site_1: 141 c 156 g 189 t
                                                                                                                                                                                                  /dev_stage="mature"
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                                                                                                                                                                                                                                                                     /clone="DCBAUC01"
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                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                        25.7%;
                                                                        Score 185.2; DB 9
Pred. No. 1.4e-24;
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ne DCBAUC01 5', mRNA sequence
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359 ttctcqaaaaagttatatgggggctgaatgagcttctggaggccttgtttaccgtttttta 418

1 AATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCT

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61 TTCTCGAAAAAGTTATATGGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTA 120

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299 aataagtcagcaccgaagcagtggttaagccggagggctcggaagaacggcaccttttct 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI838027 828 bp mRNA linear EST 04-OCT-2001 603083875F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222802 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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BI838027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11560 row: f column: 19
                                                                                    Similarity
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                                                                                                                                                                                         253
                                                                Conservative
                                                                                                                                                                                                    /note="Organ: pooled pancreas and spleen; Vector:
/note="Organ: pooled pancreas and spleen; Vector:
pcMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(ECORV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/clone="IMAGE:5222802"
/clone_lib="NIH_MGC_120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
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Pred. No. 5.6e-24;
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Search completed: September 7, 2002, 14:51:33 Job time: 16192 sec

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BB573416 BB573416 BM420516 U013C07 O BG410123 S10-8 A10 BB630820 BB630820 BH393256 AG-ND-165 AL575246 AL575246 AL575246 AL575246 AL575246 AL575246 AL57125 AL551725 A2766513 IM0564407 AA400303 zu64403 r BF835617 RC4-HT089 BF994308 CM2-GN016 AZ719811 RPCI-24-1 BB508020 BB508020 D60325 HUM099E06A AW879474 PW0-OT001 BF994425 CM2-GN016 AZ231468 RPCI-23-6	cted by chance to have a core the result being printed, score distribution.  Description			27472414		ompugen Ltd. ; Search time 8462.63 Seconds (without alignments) 31.898 Million cell updates/sec
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	AZ330109 IM0000FF/		E1002		200001 RDCT-23-2		M045047 CH348812	m34e00	A GOEST TO COOL	٠,		9 1003012	BB193000 BB193000		x 3000000 +00000000000000000000000000000			A0054255 Fun C1091	Dan tron	8.T096294	AC037563 Dan trod	131 COO CO COO COO COO COO COO COO COO COO	TE101086 237803 MA	Justination Using States	1		BG726816 sae27c11.	AQ173492 HS_3193_A

## 282 bp mRNA linear EST 30-NOV-2000 BB573416 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 493050IC15 5', mRNA sequence. BB573416 EST 30-NOV-2000

ALIGNMENTS

BB573416.1 GI:11469960

house mouse.

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci,P., Muramatsu,M. and Hayashizaki,Y.
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of the synthesis of full length
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki

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COMMENT
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mes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 gagatgcccaaactgtttt 20
Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.Chin;
Tel: 0086-571-86892051
Fax: 0086-571-86961525
                                                                                                       Dong, H.T., Li,D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C. A Gene Expression Screen in Oryza sativa Unpublished (2001)
                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 475)
                                                                                                                                                                                                                                                                                                                                                    BM420516 475 bp mRNA linear U013C07 Oryza sativa mature leaf library induced by sativa cDNA clone U013C07, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Site_1: Sall; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="testis"
/dev_stage="adult"
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/clone="4930501C15"
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/strain="C57BL/6J"
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                                       Zhejiang, P.R.China
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Fax: 212 327 8685
Plate: S10-8 row:
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Seq primer: SP6-22 5' ctt gat tta ggt gac act ata g 3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus.

1 (bases 1 to 677)

Altmann, C.R., Bell, E., Sczyrba, A., Pun, J., Bekiranov, S., Gaasterland, T. and Brivanlou, A.H.

Microarray-based analysis of early development in Xenopu.

Dev. Biol. 236 (1), 64-75 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory of Molecular Vertebrate Embryology The Rockefeller University
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Brivanlou, AH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG410123 677 bp mRNA linear EST 01-APR-2001 S10-8-A10 Stage 10+ Gastrula Library xenopus laevis cDNA 5' similar
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                        1230 York Avenue, New York, NY 10021, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to Xenopus EST, mRNA sequence.
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                                                                                                                 197
         Conservative
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                                                                                                                            translation initiation factor 4AIII. Development 124 4235-4242."
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                                                                                                                                                    /note-"Vector: pDH105/CS2++; Site_1: Sal I; Site_2: Not I Weinstein.D.C., Honore,E., and Hemmati-Brivanlou,A. (1997). Epidermal induction and inhibition of neural fate by
                                                                                                                                                                                                                                 /clone_lib="Stage 10+ Gastrula Library"
/dev_stage="10 - 10.5"
                                                                                                                                                                                                                                                                    /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                  /lab_host="DH5alpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="leaf"
/dev_stage="Mature stage"
/note="Vector: pSport2"
88 c 109 g 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/db_xref="taxon:4530"
/clone="U013C07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Natahiki,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e mouse tissues.
                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A130029G22"
/not-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                              /dev_stage="16 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                             /clone_lib="RIKEN full-length enriched, 16 days neonate
                                                                                                                                                                                          /tissue_type="thymus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                         This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TICR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH393256 796 bp DNA linear GSS 11-DEC-200
AG-ND-165J5.TF ND-TAM Anopheles gambiae genomic clone AG-ND-165J5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 796)
Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus
Direct Submission of BAC-end sequences from Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles gambiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Other_GSSs: AG-ND-165J5 TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                             Seq primer: M13 For Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Brendan J Loftus
                                                                                                                                                                                                                                           partial digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 a
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301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGCACCTCTTTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper cDNA went through one round of normalization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified pBluescript KS(+) after bulk excision from Lambda
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         /clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
/note="Vector: pECBAC1; Site_1: HindIII"
/note="Vector: pECBAC1; Site_1: HindIII"
                                                                     /clone="AG-ND-165J5"
                                                                                                                                 /organism="Anopheles gambiae"
                                                                                                                                                                               Location/Qualifiers
                                                                                       /db_xref="taxon:7165"
                                                                                                                   /strain="PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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94.7%;

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gardner, M. and Loftus, B.J.
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KEYWORDS
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                                                          ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                         59 GATGCCCAAACTGTTTT 75
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                            4 gatgcccaaactgtttt 20
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                                                                                                                                                AL551725 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI062YL18
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                    Homo sapiens
                                                                                                       AL551725.1 GI:12889952
                                                                                                                                          prime, mRNA sequence.
                                                                            numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: ppavspore 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
http://fulllength.invitrogen.com"
18 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91006 EVRY cedex - France
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="CS0DI062YB12"
/clone_lib="LTI_NFL006_PL2"
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                                                                                                                                                                                                                                                                                                                                                          85.0%; Score 17; DB 9; 100.0%; Pred. No. 3.7e+(
                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                          3.7e+02;
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                                                                                                                                                                 EST 16-FEB-2001
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                                                                                                                                                                                                                                                                                                                                   0;
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FEATURES
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AZ766513/c
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AUTHORS
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Best Local ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
            Class: plasmid ends
High quality sequence stop: 200.
                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0564 row: H column: 07
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                           University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                     Contact: Robert B.
                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                            plasmid inserts
                                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 bp DNA linear GSS 16-FEB-20
1M0564H07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0564H07 F, DNA sequence.
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BP 191 91006 EVRY cedex - France
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                              308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 a
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                                                                                                                                                                                         USA
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                                                                                                                                                                                         _____Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CS0DI062YL18"
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/tissue_type="placenta"
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                                                                                                    Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQUUJUJ 291 bp mRNA | linear EST 16-MAY-19: zu64a03.rl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742732 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 205.
                                                                                                                                                                                                                                                                            Washington University School of Medicine | 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA400303.1 GI:2054192
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwMA2 (gi14732114)gh AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                       est@watson.wustl.edu
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0564H07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
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/organism="Homo sapiens"
/db_xref="GDB:5929684"
/db_xref="taxon:9606"
                                                                                                            Location/Qualifiers
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Pred. No. 3.6e+02;
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SOURCE KEYWORDS

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                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-HT0890-
151100-017-ell&t3=2000-11-15&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RC4-HT0890-151100-017-ell HT0890 Homo sapiens cDNA, mRNA sequence.
BF835617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson, A.J.
                                                                                                                                                               High quality sequence start: 17
High quality sequence stop: 302.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                        +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:742732"
/clone_lib="Soares_testis_NHT"
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/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application
                                                                                  /clone_lib="HT0890"
                                                                                                        /db_xref="taxon:9606"
                                                             /dev_stage="Adult"
                                                                                                                      /organism="Homo sapiens"
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Pred. No. 3.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-GN0165-
021100-487-a03&t3=2000-11-02&t4=1)
                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 8 High quality sequence stop: 143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 314)
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CM2-GN0165-021100-487-a03 GN0165 Homo sapiens cDNA, mRNA sequence.
BF994308
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/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI ; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0165"
                                                                                                                                                                                                         /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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54 c 65 g 107 t
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Best Local Similarity

84.0%;

Pred. No. Score 16.8;

4e+02;

DB 10;

Length 314;

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                                                                          BB508020/c
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                                                                                                                                                AGAAATGCCCAAAGTGTTTT 110
BB508020
BB508020 RIKEN full-length enriched, 10 days lactation, adul female mammary gland Mus musculus cDNA clone D730015N05, mRN
                                                   BB508020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 161 row: H column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao,S., Nierman,W., Malek,J., Shatsman,S., AN Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Russell,D., de Jong,P. and Fraser,C.M. Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 322)
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                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                                                                              /cell_type="Spleen/Brain" /cell_type="Spleen/Brain" /note="Yector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; /note="Yector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pleter de Jong. The Library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="RPCI-24-161H14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
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Pred. No. 4e+02;
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN Mouse ESTs (Konno,H., et al.) Unpublished (2000)
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N. Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) | Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please visit our web site (http://genome.rtc.riken.go.jp) for
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was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." s 3 c 68 g 113 t
                                                                                                   Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="mammary gland"
/dev_stage="10 days lactation, adult"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                  prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                            contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adult female mammary gland"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched, 10 days lactation,
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                                                                                                                             . cDNA
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AW879474/c

DEFINITION RESULT 15

AW0/94/4 377 bp mRNA linear PMO-OT0019-180400-003-f04 OT0019 Homo sapiens cDNA, AW879474

mRNA sequence. EST 23-MAY-2000

0

SOURCE

ORGANISM

Homo sapiens

KEYWORDS

EST human

AW879474.1 GI:8041484

VERSION ACCESSION

REFERENCE

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 377)

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RESULT 14
D60325/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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                                1 agagatgcccaaactgtttt 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUM099E06A Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-099E06 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                 Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaic, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.
                                                                                                                                                                                                                                                                                      Otsuka Pharmaceutical Co.,Ltd 463-10 kagasuno Kawauchi-cho, Tel: 0886-65-2888 Fax: 0886-37-1035.
                                                                                                                                                                                                                                                                                                                                                                                   Fujiwara et al. (1995)
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
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                                                                                                                                                                                                                                                                                                                                                      Otsuka GEN Research Institute
                                                                                                                                                                                                                                                                                                                                                                     Contact: Tsutomu Fujiwara
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                                                              Conservative
                                                                                                                                                                                                                           /organism="Homo sapiens"
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90.0%;
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Pred. No. 4e+02;
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Search completed: September 7, 2002, 14:51:20 Job time: 16179 sec
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                                                                                                          341 AGAGACGCCCAAACTGGTTT 322
                                                                                                                                                                                                          Local Similarity hes 18; Conserv
                                                                                                                                     1 agagatgcccaaactgtttt 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7tl=st2=pM0-OT0019-180
400-003-f04st3=2000-04-18st4=1)
Seq primer: puc 18 forward
High quality sequence start: 27
High quality sequence stop: 377.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                            94 a
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                       /note="Organ: ovary; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196. 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
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Match Length
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  2036664 seqs, 1522705736 residues
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US-09-988-995-1867
US-09-988-995-1867
US-09-988-995-18551
US-09-888-492-18251
US-09-888-492-18251
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              Sequence 1262, Ap
Sequence 7482, Ap
Sequence 2734, Ap
Sequence 207146, Ap
Sequence 20716, Ap
Sequence 2716, Ap
Sequence 21743, A
Sequence 21743, A
Sequence 22947, Ap
Sequence 33057, A
Sequence 33057, A
Sequence 41983, A
Sequence 41983, A
Sequence 41983, A
Sequence 43780, A
Sequence 43780, A
Sequence 33057, Ap
Sequence 34930, A
Sequence 34930, A
Sequence 34930, A
Sequence 20906, A
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RESULT 2 US-10-105-299-7482/c US-10-105-299-7482/c Sequence 7482, Application US/10105299 GENERAL INFORMATION: APPLICANT: ROSen, et. al TITLE OF INVENTION: Human Secreted Proteins FILE REFERENCE: PS950 CURRENT APPLICATION NUMBER: US/10/105,299 CURRENT FILING DATE: 2002-03-26 UMBER OF SEQ ID NOS: 15197 Prior Application removed - See File Wrapper or Palm SOFTMARE: Patentin Ver. 2.0 SEQ ID NO 7482 LENGTH: 34547 TYPE: DNA	Query Match 100.0%; Score 20; DB 6; Length 45121; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 20; Conservative 0; Mismatches 0; Indels 0; G  Qy 1 agagatgcccaaactgtttt 20	RESULT 1  US-10-035-832-1262 ; Sequence 1262, Application US/10035832 ; Sequence 1262, Application US/10035832 ; GENERAL INFORMATION: ; APPLICANT: Morris, David ; APPLICANT: Engelhard, Eric ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER FILE REFERENCE: A-71249/RMS/DCF ; CURRENT APPLICATION NUMBER: US/10/035,832 ; CURRENT FILING DATE: 2002-07-22 ; PRIOR APPLICATION NUMBER: US 99/747,377 ; PRIOR APPLICATION NUMBER: US 99/747,377 ; PRIOR FILING DATE: 2000-12-22 ; PRIOR APPLICATION NUMBER: US 99/798,586 ; PRIOR FILING DATE: 2001-03-02 ; NUMBER OF SEQ ID NOS: 1613 ; SOFTWARE: PATENTIN VERSION 3.1 ; SEQ ID NO 1262 ; LENGTH: 45121 ; TYPE: DNA	ALIGNMENTS	15.8 79.0 2037 8 US-60-360-039-45839 Sequence 45 15.8 79.0 3627 7 US-10-010-95-6 Sequence 6, 15.8 79.0 3527 7 US-10-010-667A-6 Sequence 6, 15.8 79.0 59554 6 US-10-035-832-1214 Sequence 12 15.8 79.0 59554 6 US-10-035-832-1214 Sequence 12 15.4 77.0 25 US-09-396-196G-54633 Sequence 54 15.4 77.0 226 5 US-09-342-366A-1291 Sequence 54 15.4 77.0 226 5 US-09-442-366A-1291 Sequence 12	26 15.8 79.0 1157 1 PCT-USO2-09257-91 Sequence 94.   27 15.8 79.0 1157 1 PCT-USO2-09370-140 Sequence 194.   28 15.8 79.0 1157 1 PCT-USO2-09370-140 Sequence 185.   29 15.8 79.0 1157 7 US-10-105-299-180 Sequence 185.   30 15.8 79.0 1179 5 US-09-919-002-1295 Sequence 195.   31 15.8 79.0 1195 6 US-10-205-823-396 Sequence 395.   32 15.8 79.0 1195 6 US-10-205-823-396 Sequence 395.   33 15.8 79.0 1195 6 US-10-144-678A-878 Sequence 875.   34 15.8 79.0 1195 7 US-10-011-095-1 Sequence 195.   35 15.8 79.0 1195 7 US-10-011-095-1 Sequence 195.   36 15.8 79.0 1294 5 US-09-620-325-172 Sequence 395.   37 15.8 79.0 1294 5 US-09-620-325-172 Sequence 395.   38 15.8 79.0 1294 5 US-09-620-325-172 Sequence 395.   39 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   39 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   30 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   30 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   31 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   32 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   33 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   34 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   35 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   36 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   37 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   38 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   39 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   39 15.8 79.0 1294 5 US-09-620-325-172 Sequence 195.   30 15.8 79.0 1294 5 US-09-620-325-172 Sequence 19	•
	<u>~</u>			120	nce 91, Appl nce 140, App nce 85, Appl nce 180, App nce 1995, App nce 396, App nce 396, App nce 396, App nce 1, Appl	1

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ORGANISM: Homo sapiens

US-10-105-299-7482

Дb

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; LENGTH: 253
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700733864H1
US-09-975-254-2234
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                                                                                                                                                                                                       APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(1530)s
CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT APPLICATION NUMBER: US/09/263,191
PRIOR APPLICATION NUMBER: US/09/263,191
PRIOR FILING DATE: 1999-03-05
SEQ ID NOS: 31255
SEQ ID NOS: 31255
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                                                          Matches
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SEQ ID NO 17065
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APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15309)B
CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT ETLING DATE: 2001-10-12
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PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.0%; Score 17;
100.0%; Pred. No.
tive 0; Mismatc
                                                               Score 16.8;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.8;
Pred. No. 4:
                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7; Length 34547; 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
                                               2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                             Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 251;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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APPLICANT: Stuve, LAND J.
APPLICANT: Mullaby, Sara J.
APPLICANT: Mullaby, Sara J.
APPLICANT: Mullaby, Sera J.
APPLICANT: Mughton, Rebecca E.
TITLE OF INVENTION: FOLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: PD-1037 CIP
CURRENT APPLICATION NUMBER: US/09/540,210B
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 08/972,899
PRIOR FILING DATE: NOVEMBER: 08/395,244
PRIOR PRIOR APPLICATION NUMBER: 08/395,244
PRIOR PRIOR APPLICATION NUMBER: 08/395,244
PRIOR PRIOR APPLICATION NUMBER: 08/395,244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-540-210B-20774/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human US-10-027-632-205156
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CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/167,358

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-027-632-205156; Sequence 205156, App.; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20774, Application US/09540210B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FASTSEQ
SEQ ID NO 205156
LENGTH: 650
                                                                                                 PRIOR FILING DATE: September 27, 1990
PRIOR APPLICATION NUMBER: 60,0005,526
PRIOR FILING DATE: September 29, 1990
PRIOR APPLICATION NUMBER: 08,824,029
PRIOR FILING DATE: MARCH 25, 1997
PRIOR APPLICATION NUMBER: 05, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                      PRIOR FILING DATE: February 27, 1995
PRIOR APPLICATION NUMBER: 08/722,922
PRIOR FILING DATE: September 27, 1991
PRIOR FILING DATE: September 27, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Seilhamer, Jeffrey J. APPLICANT: Delegeane, Angelo M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09 NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 agaaatgtccaaactgtttt 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 agagatgcccaaactgtttt 20
APPLICATION NUMBER: 08/826,847
FILING DATE: April 10, 1997
                 APPLICATION NUMBER: 60/014,010 FILING DATE: March 25, 1996 APPLICATION NUMBER: 08/826,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sture, Laura L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.8;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7; Length 650;
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PRIOR APPLICATION NUMBER: 60/015,533
PRIOR APPLICATION NUMBER: 00/015,533
PRIOR APPLICATION NUMBER: 08/652,178
PRIOR FILING DATE: July 31, 1996
PRIOR FILING DATE: July 31, 1996
PRIOR PRIOR APPLICATION NUMBER: 60/0218,217
PRIOR APPLICATION NUMBER: 60/0218,217
PRIOR APPLICATION NUMBER: 08/881,589
PRIOR FILING DATE: July 31, 1996
PRIOR FILING DATE: May 23, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: JULY 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: JULY 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: JULY 31, 1995
PRIOR FILING DATE: JULY 31, 1995
PRIOR PRICATION NUMBER: 60/025,204
PRIOR APPLICATION NUMBER: 60/025,204
PRIOR PRILING DATE: JULY 31, 1996
PRIOR APPLICATION NUMBER: 60/025,204
PRIOR APPLICATION NUMBER: 60/025,217
PRIOR APPLICATION NUMBER: 60/035,144
PRIOR APPLICATION NUMBER: 60/035,145
PRIOR APPLICATION NUMBER: 60/035,145
PRIOR APPLICATION NUMBER: 60/035,145
PRIOR APPLICATION NUMBER: 60/036,144
PRIOR APPLICATION NUMBER: 60/036,175
PRIOR APPLICATION NUMBER: 60/036,175
PRIOR APPLICATION NUMBER: 60/036,817
PRIO
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RESULT 7
US-09-785-276A-2716
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: LOCATION: 31, 71, 74,
: OTHER INFORMATION: a,
US-09-540-210B-20774
                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: 158, 166, 285
; OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-2716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL Program
SEQ ID NO 20774
    밁
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR PILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2716, Application US/09785276A
                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Monaĥan, John TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF TITLE OF INVENTION: HUMAN PROSTATE CANCER FILE REFERENCE: MRI-007B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/785,276A CURRENT FILING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: 60/183,319 PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                              Matches
                                                                                                Best Local Similarity
                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schlegel. Robert
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature OTHER INFORMATION: Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 289
                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.0%;
Local Similarity 89.5%;
les 17; Conservation
172 gagaagcccaaactgcttt 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 gagatgcccaaactgtttt 20
                      2 gagatgcccaaactgtttt 20
                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                           364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
                                                                                                  79.0%;
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Pred. No. 1.5e+02;
0; Mismatches 2;
                                                                                Score 15.8; DB 5; pred. No. 1.5e+02; 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 289;
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                                                                                                                            Length 364;
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                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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US-09-785-276A-21743/c
; Sequence 21743, Application US/09785276A
                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEC ID NOS: 62232

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11885

LENCTH: 416

TYPE: DNA

ORGANISM: Homo sapiens

US-09-785-276A-11885
                                                                               NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-785-276A-11885
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 05/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/255,281 PRIOR FILING DATE: 2000-12-13
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ORGANISM: Homo sapiens
                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/785,276A CURRENT FILING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: 60/183,319 PRIOR FILING DATE: 2000-02-17 PRIOR APPLICATION NUMBER: 60/189,862 PRIOR PILING DATE: 2000-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MORAÑAN, JOHN
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
                                                               ENGTH: 440
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 gagatgcccaaactgtttt 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09785276A
                                                                                                                                                         2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.0%; Score 15.8; DB 5; 89.5%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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US-09-785-276A-27588/c
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; ORGANISM: Homo sapiens
US-09-785-276A-22947
                                                                                                          Sequence 27588, Application US/09785276A

GENERAL INFORMATION:
APPLICANT: Schlegel: Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
CURRENT FILING DATE: 2001-02-16
CURRENT FILING DATE: 2001-02-16
DEDTOR ADDITION NUMBER: 2010-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/218,862
PRIOR PELICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
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PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
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Best Local Similarity 89.5%;
Matches 17; Conservative
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PRIOR FILING DATE: 2000-12-13
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APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: LUDAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
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nes 17; Conserv
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89.5%;
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1.6e+02;
ches 2;
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PRIOR APPLICATION NUMBER: 60/211,314

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219,007

PRIOR FILING DATE: 2000-07-18

PRIOR PRIOR APPLICATION NUMBER: 60/255,281

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 62232

NUMBER OF SEQ ID NOS: 62232
US-09-785-276A-33057
; Sequence 33057, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel. Robert
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28808
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PRÉVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-0-17
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APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
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PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
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PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
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PRIOR FILING DATE: 2000-03-16
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ORGANISM: Homo sapiens
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308 GAGAAGCCCAAACTGCTTT 290
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                                                                                                                                                                                                                                                                             Score 15.8; DB 5; Pred. No. 1.6e+02;
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-785-276A-33057
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-785-276A-41983
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 33057
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PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/219,007
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Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                       NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41983
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
FILE REFERENCE: MRI-007B
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APPLICANT: Monahan, John
APPLICANT: MONAHAN, JOHN
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
FILE REFERENCE: MRI-007B
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PRIOR FILING DATE: 2000-06-09
PRIOR PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
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PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                            PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
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                                                                                     LENGTH: 451
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US-09-785-276A-43780

US-09-785-276A-43780

Sequence 43780, Application US/09785276A

Sequence 43780, Application US/09785276A

APPLICANT: Schlegel. Robert

APPLICANT: Schlegel. Robert

APPLICANT: Monahan, John

ITILE OF INVENTION: HUMAN PROSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: HUMAN PROSITIONS, KITS, AND THERAPY OF TITLE OF INVENTION: HUMAN PROSTATE CANCER

URRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US/09/785,276A

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/28,319

PRIOR APPLICATION NUMBER: 60/28,319

PRIOR APPLICATION NUMBER: 60/21,314

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR APPLICATION NUMBER: 60/215,281

PRIOR APPLICATION NUMBER: 60/215,281

PRIOR APPLICATION NUMBER: 60/215,281

PRIOR APPLICATION NUMBER: 60/255,281

PRIOR APPLICATION NUMBER: 60/251,314

PRIOR APPLICATION
Search completed: September 8, 2002, 01:09:18 Job time: 37036 sec
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Best Local Similarity 89.5%;
Matches 17; Conservative (
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174 gagaagcccaaactgcttt 192
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels (
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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APPLICANT: Kunner, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: 953 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: DE 1989/10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEO ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
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SEQ ID NO 12
LENGTH: 20
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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-09-834-291-12
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
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                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 32; Length 20; 100.0%; Pred. No. 6.5;
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17 US-09-342-216A-31

18 US-09-908-601-31

34 US-09-912-292-1183

18 US-09-912-292-1183

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PCT-US02-03987-6707
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SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 26
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TYPE: DNA
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US-09-834-291-26
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; TYPE: DNA
; ORGANISM: HOMO Sapiens
US-09-834-291-4
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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
ITILE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1998-10-18
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
Query Match 100.0%; Score 20; DB 32; Length 2827; Best Local Similarity 100.0%; Pred. No. 18; Matches 20; Conservative 0; Mismatches 0; Indels 0
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PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR APPLICATION NUMBER: DE 198 47 779.1
NUMBER OF SED ID NOS: 32
COUNTRE SED ID NOS: 32
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB: 100.0%; Pred. No. 7.5; tive 0; Mismatches
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Gaps

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Sequence 10, Application US/09997722

SEMERAL INFORMATION:
APPLICANT: MORRIS, David
APPLICANT: MORRIS, David
APPLICANT: MORRIS, David
APPLICANT: MORRIS, DETIC
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS, FOR CANCER
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/748,586
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER: OF SEQ ID NOS: 301
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US-09-834-291-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-997-722-10
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                                                                                                                                                                                                                                                                     ; TYPE: DNA; ORGANISM: Homo sapiens US-09-997-722-10
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; Sequence 719, Application US/09910943
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PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
                    US-09-910-943-719/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                           Matches
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                                                                                             8037 agagatgcccaaactgtttt 8056
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; LOCATION: (1)..(732) ; OTHER INFORMATION: n may be a or g or c or t/u US-09-910-943-719
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APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Altman, Curtis
TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
TITLE REPERENCE: 7529/1G148US1
FILE REPERENCE: 7529/1G148US1
CURRENT APPLICATION NUMBER: US/09/910,943
CURRENT FILING DATE: 201-07-23
NUMBER OF SEQ ID NOS: 742
SOFTWARE: PatentIn version 3.1
SEQ ID NO 719
SEQ ID NO 719
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                                                                              Sequence 1, Application US/09438185

SEQUENCE I, Application US/09438185

APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Bavis, Ronald
APPLICANT: Davis, Ronald
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
FITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FITLE REFERENCE: 018941-000411US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 596, Application US/09528237A
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
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Best Local Similarity
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TITLE OF INVENTION:
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CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 2926
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CURRENT APPLICATION NUMBER: US/09/438,185
CURRENT FILING DATE: 1999-11-11
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GAGATGCCCAAACTGTTCT 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Conservative
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Venter, J. Craig

NVENTION: The Drosophila Genome, Primary Nucleic

NVENTION: Acid Sequences, Systems Containing The Nucleic Acid

NVENTION: Sequences and Uses Thereof

NNCE: CL000284
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94.7%;
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-0
NUMBER OF SEQ ID NOS: 107

1999-04-08

US 60/128,606

1074

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APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
ITILE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
CURRENT FILING DATE: 1902-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/128,606
NUMBER OF SEQ ID NOS: 1074
SOFTMARE: FastSEQ for Windows Version 3.0
LEMETH: 1330730
                                                                                                                                                                                                                                             US-09-815-264-56014/c
Sequence 56014, Application US/09815264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   Db 1024745 GAGATGCCAAAACTGTTTT 1024727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-438-185A-1
APPLICANT: WCININCH, James
APPLICANT: WL, Wei
TITLE OF INVENTION: Genomic Plant Sequences and Uses Thereof
FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                            APPLICANT:
                                                                                                                                                                                                            APPLICANT: Boukharov, Andrey A. APPLICANT: Cao, Yongwei
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                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Chlamydia pneumoniae
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Dotson, Stanton B
Koshi, Jeffrey M.
Kovalic, David K.
                                                                                                                                          Liu, Jingdong
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94.7%;
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; TYPE: DNA; ORGANISM: Oryza sativa US-09-702-134-2703
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FUNCTH: 7865

FYPE: DNA

ORGANISM: OTYZA SATÍVA

US-09-620-392-50130
      Best Local Similarity 100.0%; F Matches 17; Conservative 0;
                                                                                                                                  NUMBER OF SEQ ID NOS:
SEQ ID NO 2703
LENGTH: 7865
                                           Query Match
                                                                                                                                                                                                                                                                                                                                    Sequence 2703, Application US/09702134 GENERAL INFORMATION
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                                                                                                                                                                          FILE REFERENCE: 38-21(51237)F
CURRENT APPLICATION NUMBER: US/09/702,134
CURRENT FILING DATE: 2000-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE OF INVENTION: Plant Genome Sequence And Uses Thereof FILE REFERENCE: 38-21(51237)E CURRENT APPLICATION NUMBER: US/09/620,392 CURRENT FILING DATE: 2000-07-19
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TITLE OF INVENTION: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boukharov, Al APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 56014
LENGTH: 1501
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Best Local
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                                                                                                                                                                                                                                                                                  Cao, Yongwei
Kovalic, David K.
                                                                                                                                                                                                                                                        McIninch, James
                                                                                                                                                                                                                                                                        Liu, Jingdong
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              85.0%; Score 17; DB 28; Length 7865; 100.0%; Pred. No. 8e+02;
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Mismatches

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; ORGANISM: Oryza sativa
US-09-815-264-82703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 82703
LENGTH: 7865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5331, Application US/09950083
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TITLE OF INVENTION: Genomic Plant Sequences And Uses
FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
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                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/833,245
                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: PCT/US01/11988
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: PCT/US00/06043
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/950,083
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                                                                         OR APPLICATION NUMBER: PCT/US00/06058
OR FILING DATE: 2000-03-09
OR APPLICATION NUMBER: PCT/US00/06044
OR FILING DATE: 2000-03-09
OR APPLICATION NUMBER: PCT/US00/06059
OR FILING DATE: 2000-03-09
OR APPLICATION NUMBER: PCT/US00/06042
OR APPLICATION NUMBER: PCT/US00/06042
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FILING DATE: 2000-03-09
APPLICATION NUMBER: PCT/US00/06014
FILING DATE: 2000-03-09
APPLICATION NUMBER: PCT/US00/06013
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Kovalic, David K.
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PRIOR APPLICATION NUMBER: PCT/US00/06049
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APPLICATION NUMBER: PCT/US00/06057
FILING DATE: 2000-03-09
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APPLICATION NUMBER: PCT
FILING DATE: 2000-03-16
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FILING DATE: 2000-03-16
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APPLICATION NUMBER: PCT/US00/06792
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FILING DATE: 2000-03-22
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                                                                                                           APPLICATION NUMBER: PCT/US00/09070 FILING DATE: 2000-04-06 APPLICATION NUMBER: PCT/US00/08982
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              APPLICATION NUMBER: PCT/US00/09067 FILING DATE: 2000-04-06
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FILING DATE: 1999-06-11
APPLICATION NUMBER: US 60/168,665
                                                                        APPLICATION NUMBER: US 60/124,095 FILING DATE: 1999-03-12
                                                APPLICATION NUMBER: US 60/138,598
                                                                                                                 APPLICATION NUMBER: US 60/168,663 FILING DATE: 1999-12-03
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FILING DATE: 1999-12-03
APPLICATION NUMBER: US 60/124,099
FILING DATE: 1999-03-12
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APPLICATION NUMBER: PCT/US00/26337
FILING DATE: 2000-09-26
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FILING DATE: 2000-09-26
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APPLICATION NUMBER: PCT/US00/26371
FILING DATE: 2000-09-26
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FILING DATE: 2000-06-01
APPLICATION NUMBER: PCT/US00/14973
FILING DATE: 2000-06-01
APPLICATION NUMBER: PCT/US00/14964
FILING DATE: 2000-06-01
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APPLICATION NUMBER: PCT/US00/15136
FILING DATE: 2000-06-01
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APPLICATION NUMBER: PCT/US00/14933
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FILING DATE: 2000-04-06
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PRIOR FILING DATE: 1999-12-03
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                                                                                        Local Similarity hes 17; Conserv
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FILING DATE: 1999-06-11
APPLICATION NUMBER: US 60/168,662
FILING DATE: 1999-12-03
APPLICATION NUMBER: US 60/124,144
FILING DATE: 1999-03-12
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FILING DATE: 1999-06-11
APPLICATION NUMBER: US 60/168,667
FILING DATE: 1999-12-03
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APPLICATION NUMBER: US 60/125,360
FILING DATE: 1999-03-19
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Search completed: September 7, 2002, 22:31:31 Job time: 43785 sec

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Maximum DB seq length: 2000000000
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and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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TELEFAX: (650)493-5550
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:

w

SEQUENCE CHARACTERISTICS:
LENGTH: 661 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

FEATURE:

NAME/KEY: CDS LOCATION: 1 .. 660 TOPOLOGY: linear MOLECULE TYPE: DNA

UR S I S T S I S	0000 0 00	
OULT	44444 5444 544 544 544 544 544 544 544	
OB-578-634C-3/C  Gequence 3, Application US/08578634C  attent No. 6025163  attent No. 6025163  APPLICANT: Vladimir Shamanin APPLICANT: Ethel Michele De Villiers APPLICANT: Ethel Michele De Villiers APPLICANT: Irene Leigh APPLICANT: Harald Zur Hausen APPLICANT: Horen Leigh APPLICANT: Harald Zur Hausen APPLICANT: Horen Leigh APPLICANTON USA ZIP: 10036 COUNTRY: USA ZIP: 10036 COUNTRY: USA ZIP: 10036 COMPUTER: Horen Leigh APPLICATION NUMBER: Horen Leigh APPLICATION NUMBER: Horen Leigh APPLICATION NUMBER: Horen Leigh APPLICATION LEIGH COMPUTER: Horen Leigh APPLICATION LEIGH COMPUTER: Horen Leigh APPLICATION LORGE: Horen Leigh APPLICANTON LORGE: Horen Leigh APPLICANTON LORGE: Horen Leigh COMPUTER: Horen Leigh APPLICANTON LORGE: Horen	14.4 72.0 9103 1 US-08-444-733-182 Sequence 14.4 72.0 9103 2 US-08-461-361-182 Sequence 14.4 72.0 9103 2 US-08-461-361-182 Sequence 14.4 72.0 9103 2 US-08-485-910-182 Sequence 14.4 72.0 9103 2 US-08-485-910-182 Sequence 14.2 71.0 612 4 US-09-385-982-64 Sequence 14.2 71.0 612 4 US-09-385-982-64 Sequence 14.2 71.0 756 5 PCT-US96-03940-2 Sequence 14.2 71.0 1067 4 US-08-858-207A-104 Sequence 14.2 71.0 1255 4 US-09-287-357-52 Sequence 14.2 71.0 1255 PCT-US96-03940-3 Sequence 14.2 71.0 1264 S PCT-US96-03940-3 Sequence 14.2 71.0 1461 S PCT-US96-03940-3 Sequence 14.2 71.0 1451 S PCT-US96-03940-3 Sequence 14.2 71.0 1452 S PCT-US96-03940-3 Sequence 14.2 71.0 1451 S PCT-US96-03940-3 Sequence 14.2 71.0 1451 S PCT-US96-03940-3 Sequence 14.2 71.0 1452 S PCT-US96-03940-3 Sequence 14.2 71.0 1452 S PCT-US96-03940-3 Sequence 14.2 71.0 1757 2 US-08-453-848-14 Sequence 14.2 71.0 1757 2 US-08-453-848-14 Sequence	
	182, App 182, App 182, App 182, App 182, App 156, App 11, Appl 15, Appli 104, Appli 20, Appli 21, Appli 22, Appli 3, Appli 3, Appli 3, Appli 14, Appl	
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US-08-578-634C-3

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RESULT 3
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SEQUENCE CHARACTERISTICS:
LENGTH: 43795 base pairs
TYPE: nucleic acid
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FILING DATE: 31-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 101, App.
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                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                              1 agagatgcccaaactgtttt 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DA2: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                             Local Similarity
                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI94-07A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Lexington STATE: Macon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 567 AGAGTTGCCCAAAGTGTTTT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/742,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 agagatgcccaaactgtttt 20
                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saxena, Richa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reijo, Renee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page, David C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-OCT-1996
                                                                                                         84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.0%;
90.0%;
                                                                                          0; Mismatches
                                                                                                         Score 16.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 4.7;
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                                                                                                      10;
                                                                                                                 DB 3; Length 43795;
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APPLICANT: Arthur B. Raitano

APPLICANT: Douglas C. Saffran

APPLICANT: Steve Chappell Mitchell

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF

FILE REFERENCE: 129.16USU2

CURRENT APPLICATION NUMBER: US/09/323,873A

CURRENT FILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 32

SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
RepLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitan
APPLICANT: Douglas C. Saffr
APPLICANT: Steve Chappell M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-323-873A-6/c
                                                  Matches
                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                  SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-323-873A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09323873A Patent No. 6329503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-323-873A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                              LENGTH: 3627
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APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
FILE REFERENCE: 129.16USU2
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APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raita
2 gagatgcccaaactgtttt 20
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                                               al Similarity
17; Conserv
                                           Conservative
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                                                            79.0%;
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89.5%; Pred. No. 18;
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                                0; Mismatches
                                                          Score 15.8;
Pred. No. 22;
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                                                                          DB 4;
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                                     2;
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                                                                       Length 3627;
                                     Indels
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                                0;
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                                Gaps
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596 GAGAAGCCCAAACTGCTTT 578

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RESULT 5
US-07-903-047-7/c
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                                                                                                                                                                                                                                                                                       US-09-111-752-13/c
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                                                                                                                                                                                                                                              Sequence 13, Appli
Patent No. 6074859
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kajiyama, Naoki
APPLICANT: Nakano, Eiichi
TITLE OF INVENTION: Thermostable Luciferase Of Firefly, No. 5229285el Recombi
TITLE OF INVENTION: Thermostable Luciferase Gene Of Firefly, No. 5229285el Recombi
TITLE OF INVENTION: DAA, And Process For The Preparation Of Thermostable
TITLE OF INVENTION: Luciferase Of Firefly
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                           GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                               APPLICANT: HIROKAWA, KOZO
APPLICANT: KAJIYAMA, NAOKI
APPLICANT: MURAKAWI, SELJI
TITLE OF INVENTION: MUTANT-TYPE BIOLUMINESCENT PROTEIN, AND
TITLE OF INVENTION: PROCESS FOR PRODUCING MUTANT-TYPE LUMINESCENT PROTEIN
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                     369 AGAGATGCCTAAACTGT 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                     ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                          1 agagatgcccaaactgt 17
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRY: U.S.A.
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 1644 base pairs
NUCLEIC ACID
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1155 Avenue of the Americas
                                                                                                                                                                                                                                                                    Application US/09111752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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94.1%;
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Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1644;
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ORGANISM: Luciola lateralis US-09-111-752-13
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Sequence 15, Application US/09380061B
Patent No. 6265177
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity Matches 16; Conserv
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NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/09/380,061B
FILING DATE: 25-Aug-1999
CLASSIFICATION LOTA
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 AGAGATGCCTAAACTGT 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SQUIRRELL, DAVID JAMES
WHITE, PETER JOHN
LOWE, CHRISTOPHER ROBIN
LOWE, CHRISTOPHER ROBIN
MURRAY, JAMES AUGUSTUS HENRY
TITLE OF INVENTION: ENZYME ASSAY FOR MUTANT FIREFLY LUCIFERASE
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON
                  APPLICATION NUMBER: PCT/GB98/01026
FILING DATE: 7-APR-1998
APPLICATION NUMBER: GB 9707468.8
FILING DATE: 11-APR-1997
                                                                                                                                                                                                                                                                                                                           STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: NIXON & VANDERHYE P.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.0%; Score 15.4;
94.1%; Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
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NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663

124-725

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US-08-460-934-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5814465
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08460934 Patent No. 5814465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
                                                   ATTORNEY/AGENT INFORMATION:
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,934
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: AN NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703)816-4100 INFORMATION FOR SEQ ID NO: 15:
                    NAME: OBLON, NORMAN F. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                         FILING DATE:
   REFERENCE/DOCKET NUMBER:
                                                                             FILING DATE:
                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 AGAGATGCCTAAACTGT 353
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l agagatgcccaaactgt 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
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                                                                                                                                                                                                                                                                                                                                                                                           22202
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1644 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIKUCHI, MAMORU
KOYAMA, YASUJI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                       UMBER: JP 98857/1995
24-APR-1995
                                                                                                                       UMBER: JP 54625/1995
14-MAR-1995
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94.1%;
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                  24,618
7126-001-0
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Pred. No. 31;
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US-08-782-118-5/c
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TELEPAN: 703-413-2220
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08782118 Patent No. 5843746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KIKUCHI,
APPLICANT: KOYAMA, Y
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 14-MAR-
                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                     ZIP: 22202
COMPUTER READABLE FORM:
TRATIM TYPE: Floppy disk
                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                               APPLICATION NUMBER: US 08/460,934
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: JP 193798/199
FILING DATE: 27-JUL-1994
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 22202
                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 13-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429 AGAGATGCCTAAACTGT 413
                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
COMPUTER: IF
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1..1704
OTHER INFORMATION: /note= "Nucleotide sequence of the
OTHER INFORMATION: biotinylated firefly luciferase gene contained in recombin
OTHER INFORMATION: plasmid phif203 DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 agagatgcccaaactgt 17
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FUKUDA, SATOSHI
KIKUCHI, MAMORU
KOYAMA, YASUJI
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                                                     UMBER: JP 54625/1995
14-MAR-1995
24-APR-1995
                                                                                                                                                                                                             13-JAN-1997
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94.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOTINYLATED FIREFLY LUCIFERASE, A GENE FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANALYSIS METHOD
14
                JP 98857/1995
                                                                                                                       JP 193798/1994
                                                                                                                                                                                                                        US/08/782,118
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Pred. No. 31
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US-08-782-118-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..1704
OTHER INFORMATION: /note
OTHER INFORMATION: bioti
OTHER INFORMATION: plasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTI
TITLE OF INVENTION: FOR BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429 AGAGATGCCTAAACTGT 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                  FILING DATE: 27-JUL-:
PRIOR APPLICATION DATA:
                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: JP 193798/1994
APPLICATION NUMBER: JP 193798/1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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FILING DATE: 14-MAR-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                    APPLICATION NUMBER: US/08/460,934
                                                                                                                                  FILING DATE: 05-JUN-1995
                  APPLICATION NUMBER: JP 54625/1995 FILING DATE: 14-MAR-1995
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1755 S. JEFFERSON DAVIS HIGHWAY, FOURȚH FLOOR
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KIKUCHI, MAMORU
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                                                                                                                                                                                                                                                                                               USA
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                                                                  27-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                 ANALYSIS METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.0%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOTINYLATED FIREFLY LUCIFERASE, A GENE
FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Nucleotide sequence of the
biotinylated firefly luciferase gene contained in recombinant
plasmid pHLf203 DNA" |
                                                                                                                                                                                                                                                                                                                                                                                                                    14
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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US-08-460-934-8
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: TATSUM
APPLICANT: FUKUDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
   PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/460,934
APPLICATION NUMBER: US 08/460,934
APPLICATION TIMES TO 19193798/1994
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 AGAGATGCCTAAACTGT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 1..1908 OTHER INFORMATION: /not OTHER INFORMATION: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 77.0%; Local Similarity 94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 agagatgcccaaactgt 17
                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C.
                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                               CITY: ARLINGTON
                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                 COUNTRY:
                                                                                          FILING DATE:
FILING DATE:
                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                           3: P.C.
1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUKUDA, SATOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
                                                                                                                                                                                      Floppy disk
                                                                                          13-JAN-1997
                                                                                                                                                                                                                                                                                                                                                           BIOTINYLATED FIREFLY LUCIFERASE, A GENE
FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
ANALYSIS METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "The nucleotide sequence of
the biotinylated firefly luciterass
recombinant plasmid pHLf248 DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIROKI
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                                                                                                            US/08/782,118
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Pred. No. 32
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PRIOR APPLICATION DATA:

FILING DATE: APPLICATION NUMBER:

14-MAR-1995

JP 54625/1995

JP 98857/1995

PRIOR APPLICATION DATA:

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US-08-578-634C-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 16; Conserv
                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,634C
FILING DATE: 26-JAN-1996
                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Irene Leigh
APPLICANT: Harald Zur Hausen
TITLE OF INVENTION: DNA CODING FOR A PEPTIDE OF A PAPILLOMA
TITLE OF INVENTION: VIRUS MAIN CAPSIDE PROTEIN AND USE THEREOF
                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                            MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 AGAGATGCCTAAACTGT 353
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FILING DATE:
              APPLICATION NUMBER:
                                                                                                                                                                                                                                     CITY: New York
STATE: New York
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LENGTH: 1908 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 90
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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OTHER INFORMATION:
OTHER INFORMATION:
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 71:
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                                                                                                                                                                                                          10036
                                                                                                                                                                                                                                                                1155 Avenue of The Americas
                                                                                                                                                                                                                      USA
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94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "The nucleotide sequence of
the biotinylated firefly luciferase gene contained in
recombinant plasmid pHLf248 DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.4;
Pred. No. 3
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RESULT 13
US-09-109-204-20/c
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             INFORMATION FOR SEQ ID NO:
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Patent No.
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                                                   NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39.132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 493-4935
TELEFAX: (650)493-5556
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                               TELEX:
                                          TELEFAX: 650-855-0572
                                                                                                                                              FILING DATE
                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                  ZIP:
                                                                                                                                                                                                                                                                                                                                               STREET: 3174 POI
CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 17; Conserv
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lo. 6060250
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Gorgone, Ginc.
Corley, Neil C.
F: Patterson, Chandra
Franton: HUMAN TRANSFERASES
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Hillman, Jennifer L.
Guegler, Karl J.
                                                                                                                                                                                                                                                                     IBM Compatible
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                                                                                PF-0546 US
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IMMEDIATE SOURCE:
; LIBRARY: TESTNOT04
; CLONE: 301251T6
US-09-109-204-20
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                                       US-09-109-204-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Query Match
                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 605 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WORD Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Patterson, Chandra TITLE OF INVENTION: HUMAN TRANSFERASES NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 AGATGGCCAAACTGTATT 328
                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
CITY: F
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                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                         NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                          TOPOLOGY:
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Hillman, Jennifer L.
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Pred. No. 51
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 Score 14.8;
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 Length 605;
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RESULT 15
US-09-109-204-5
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US-09-109-204-5
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                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                      NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN TRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2125 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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1780 AGATGGCCAAACTGTATT 1797
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Hillman, Jennifer L.
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Pred. No. 67
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Search completed: September 7, 2002, 18:21:07 Job time: 28761 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*
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                                Chromosome 13q31-q
Human reproductive
                                                                                                                                                                          Human CD95 recepto
Enterococcus faeca
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                                                                                                      Papilloma virus ma
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                                                                                                                                                      Enterococcus
               reproductive
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.4 77.0 2019 17 AAT 338	.4 77.0 1920 19 AAV3246	.4 77.0 1908 18 AAT6326	.4 77.0 1704 19 AAV2	5.4 77.0 1704 18 AAT6326	.4 77.0 1656 20 AAX2571	77.0 1644 20 AAX25	.4 77.0 1644 20 AAX8439	.4 77.0 1644 20 AAX8439	.4 77.0 1644 14	.4 77.0 1644 11	.4 77.0 496	.4 77.0 150 21	.8 79.0 32172 22	.8 79.0 16989	.8 79.0 6396 23	.8 79.0 4005 23	.8 79.0 3627 22	.8 79.0 3627 21	.8 79.0 3123 23	.8 79.0 2757 24	.8 79.0 2516 23	.8 79.0 2108 24 ABA	.8 79.0 2005 23	79.0 1294 22	8 79.0 1229 22 AAK!	8 79.0 1227 23 AAS!	8 79.0 1195 22 AAHS	8 79.0 1195 22 AASI	5.8 79.0 1193 22 AADO	5.8 79.0 1193 21 AAZ4	.8 79.0 1157 22 AAF638	6.4 82.0 396 22 AAH99	6.8 84.0 349980 22 AAH4122	0.0
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## ALIGNMENTS

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AAZ88701
ID AAZ
RESULT
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                                                                                                                                                                                                          p53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                                             Human CD95 receptor promoter DNA p53 binding fragment #1.
                                                                                                                                                                                                                                                                       AAZ88701;
                                                                                                                                                                                                                                                   11-MAY-2000 (first entry)
      Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy \dot{\ }
                                                        Krammer P, Mueller-Schilling M, Oren M;
                                                                                                                                         03-FEB-2000
                                                                                                                                                             DE19847779-C1.
                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                  cancer chemotherapy; ss.
                                     WPI; 2000-162245/15.
                                                                             (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                  16-OCT-1998;
                                                                                                                    16-OCT-1998;
                                                                                                  98DE-1047779
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Claim 2;

Fig 5; 12pp; German.

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RESULT 2
AAS51323/c
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          The invention relates to antisense inhibitors of genes essential to genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are pneumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets to identify proteins used in proliferation, to express these proteins, and invention is also useful for the identification of potential new targets to identify proteins used in proliferation, to express these proteins, and the control of potential new targets to identify proteins used in proliferation, to express these proteins,
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to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
                                                                                                                                                             Claim 27; Seq ID No 3905; 511pp; English.
                                                                                                                                                                                     antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                    New polynucleotides for the identification and development
                                                                                                                                                                                                                                          P-PSDB; AAU33464.
                                                                                                                                                                                                                                                                                                 Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2000;
23-MAY-2000;
                                                                                                                                                                                                                                                                                     Yamamoto RT,
                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; ds; prokaryotic cellular proliferation gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis DNA for cellular proliferation protein #100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibiotic; antibacterial; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS51323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS51323 standard; DNA; 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor promoter which is capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 agagatgcccaaactgtttt 20
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                                                                                                                                                                                                                                                       2001-611495/70
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                                                                                                                                                                                                                                                                                                                                                                                  2000US-207727P.
2000US-242578P.
2000US-253625P.
                                                                                                                                                                                                                                                                                                                                                   2001US-269308P
                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-191078P.
2000US-206848P.
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                                                                                                                                                                                                                                                                                                                                                                      2000US-257931P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                    Xu HH;
                                                                                                                                                                                                                                                                                                Ohlsen
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                                                                                                                                                                                                                                                                                           Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               design
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                                                                                                                                                                                                                                                                                           Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
.57;
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                                                                                                                                                                                                                                                                                        Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                           · of
                                                                                                                                                                                                                                                                                        Carr GJ;
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AAS53070,
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                                                                                                                                                                                                                                                                                                                             21-MAR-2000; 2000US-191078P.
23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-42578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                         Claim 27; Seq ID No 6707; 511pp; English.
                                                                                                                                                                          antibiotics, comprise sequences of
                                                                                                                                                                                                                       P-PSDB; AAU35211.
                                                                                                                                                                                                                                                                              Haselbeck R,
                                                                                                                                                                                                                                                                 Yamamoto RT,
                                                                                                                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecalis DNA for cellular proliferation protein #498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; ds; prokaryotic cellular proliferation gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS53070 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS53070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 234 BP; 84 A; 33 C; 46 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                polynucleotides for the identification and development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 AGAAATGCACAAACTGTTTT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 agagatgcccaaactgtttt 20
                                                                                                                                                                                                                                    2001-611495/70
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proteins used in proliferation, to express these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                              Ohlsen
                                                                                                                                                                                                                                                               Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306
                                                                                                                                                                                                                                                                        Zyskind JW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                          antisense
                                                                                                                                                                                                                                                                        Wall D,
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                                                                                                                                                                       nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234;
                                                                                                                                                                                                                                                                    Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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proteins,

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RESULT
AAC18125
The present sequence is one of a large number of 5' ESTs derived from CC identified within the present sequence. The 5' ESTs were prepared from CC identified within the present sequence. The 5' ESTs were prepared from CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST CC sequences usually correspond mainly to the 3' untranslated region (UTR) CC sequences usually correspond mainly to the 3' untranslated region (UTR) CC libraries. Such ESTs are not well suited for isolating cDNA sequences CC libraries. Such ESTs are not well suited for isolating cDNA sequences country in the sequences have been obtained, the full 5' UTR is rarely included. CC CDNA sequences have been obtained, the full 5' UTR is rarely included. CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design CC expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide wariety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 306 BP; 117 A; 40 C; 65 G; 84 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC18125 standard; cDNA; 338 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein 5' EST, SEQ ID NO: 22200.
                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dumas Milne Edwards J, Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 AGAAATGCACAAACTGTTTT 86
                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID 22200; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 agagatgcccaaactgtttt 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; Ss.
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.8;
Pred. No. 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
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                                                                                                 Query Match
Best Local :
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 밁
                                                     Query Match
Best Local 9
                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 338 BP; 86 A; 60 C; 42 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT03501 standard; DNA; 661 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Papilloma virus major capsid protein DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT03501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             skin carcinomas; therapy; vaccination; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HP-Virus 49; papilloma virus; major; capsid protein; plasmid VS40-7; DSM
                                                                                                                                                                                                                                                                                                                                                            04-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Papilloma virus.
                                                                                                                                                                                                                                                                                                                                      04-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                        DE4415743-A1
                                                                                                                               peptide of papilloma virus (PV) major capsid protein and is expressed by the plasmid VS40-7 (DSM 9135). The DNA is useful in diagnosis, esp. to detect PV in skin carcinomas. Major capsid proteins encoded by a PV genome contg. the DNA are useful for
                                                                                                                                                                                                                                                                                           de Villiers zur Hausen E,
                                                                                                                                                                                                                                                                                                               (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                            AAT03501 is 78.5% homologous to HP-Virus 49, encodes AAR88269 a
                                                                                                                                                                                                                        useful
                                                                                                                                                                                                                                  DNA encoding peptide(s) of papilloma virus major capsid
                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                Sequence 661 BP; 195 A; 118 C; 155 G; 193 T; 0 other;
                                                                                                                                                                                                   Claim 1; Fig 3; 15pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 agaaatggccaaactgtttt 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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 567
                                                      Local Similarity
                     1 agagatgcccaaactgtttt 20
                                                                                                                                                                                                                                                                      1995-383680/50
AGAGTTGCCCAAAGTGTTTT 548
                                                                                                                                                                                                                        for detecting papilloma virus in skin carcinoma
                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR88269
                                                                                                                        and/or vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                            Conservative
                                                                                                                                                                                                                                                                                                                                        94DE-4415743
                                                                                                                                                                                                                                                                                                                                                               94DE-4415743
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0%;
                                                         84.0%;
                                                                                                                                                                                                                                                                                              Leigh I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.8;
Pred. No. 4
                                                          Score 16.8; DB 16;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSM 9135;
                                                  Mismatches
                                                                                                                                                                                                                                                                                                Shamanin V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                 zur Hausen H;
                                                                       Length 661;
                                                    Inde'ls
                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                    0
                                                    Gaps
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AAV39297 RESULT

0

AAV39297 standard; cDNA; 2008 BP

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RESULT ...
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                                                                                                                                                                                                                                                                     The present sequence represents a specifically claimed partial nucleic acid sequence encoding human RAD54 (hRAD54). A method for analysing a CC sample for mutation of DNA encoding hRAD54 has been developed using a CC DNA sequence of at least 15 and no more than 30 consecutive bases of the DNA sequence encoding hRAD54. hRAD54 is a gene thought to be present identified as one of four minimal regions of chromosome 1 deletion in CC alia, that have been identified as novel hRAD54 is or production of proteins, inter CC amino acid sequence given in AAW62186 and known amino acid sequences cCC cancer, including Xeroderma Pigmentosum and Bloom syndrome, Werner's CC syndromes and X-linked mental retardation with alpha-thalassaemia CC detecting complementary nucleotides for use as a diagnostic agent, cc especially useful for diagnosis of disease or susceptibility to diseases. XXX proteins are useful in gene therapy.
 29-AUG-2001
                                                   AAH51750 standard; DNA; 3001 BP
                               AAH51750;
                                                                                                                                                                                                                                                Sequence 2008 BP; 489 A; 419 C; 570 G; 526 T; 4 other;
                                                                                                                         139 agagatgcccaaactgagtt 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 27-28; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human hRAD54 DNA and polypeptide - and agonists, antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antagonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-274189/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; RAD54; hRAD54; cancer; xeroderma pigmentosum; Bloom syndrome; werner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily; X-linked mental retardation with alpha-thalassemia syndrome; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP844305-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human RAD54 nucleic acid sequence comprising exons 5-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-1998 (first entry)
                                                                                                                                                  1 agagatgcccaaactgtttt 20
                                                                                                                                              Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fishel RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0030676
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                                                                                                                                                                                                84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rasio D,
                                                                                                                                                                                  0;
                                                                                                                                                                                              Score 16.8;
Pred. No. 57;
                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                          DB 19;
                                                                                                                                                                                                         Length 2008;
                                                                                                                                                                             0,
                                                                                                                                                                            Gaps
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Claim 2; Page 643-644; 737pp; English.
                                 Polynucleotides comprising sequences from sbg1 and g35018 biallelic markers are used for genotyping and detecting schizophrenia or bipolar disorder and predisposition to these disorders -
                                                                                                                                  WPI; 2000-619082/59.
                                                                                                                                                                                                   Cohen D,
                                                                                                                                                                                                                                       (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                         30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                            27-JUL-1999;
29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                         14-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sbg1; g34665; sbg2; g35017; g35018; chromosome 13g31-q33; haplotype;
biallelic marker; polymorphism; schizophrenia; bipolar disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosome 13q31-q33 biallelic marker containing amplicon SEQ ID 162.
                                                                                                                                                                                               Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                          99US-0126903.
99US-0131971.
99US-0132065.
99US-0143928.
99US-0145915.
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                                                                                                                                                                                                                                                                                                    99US-0146452.
99US-0146453.
                                                                                                                                                                                 Chumakov I, Bougueleret L,
                                                                                                                                                                                        Bihain
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AAH51601 represents a human genomic nucleotide sequence comprising sbg1, CC g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the CC human chromosome 13g31-g33 locus. The nucleotide sequences contain CC hab62907 - AAB62915 represent cDNA human sbg1 cDNA sequences and polymorphisms. Sequences AAH51602 - AAH51626 and CC products. AAH51627 - AAH51621 and AAB62916 - AAB62918 represent g35018 CC cDNA sequences and protein products. Primers AAH51632 - AAH51699 are used CC crown sequences and protein products. Primers AAH51632 - AAH51699 are used CC camplicons which comprise biallelic markers located on the chromosome CC amplicons which comprise biallelic markers located on the chromosome CC are represented in the sequences by degenerate/undefined base codes. PCR cc is a sequence of the invention. The biallelic marker containing nucleotide sequences of CC used to determine the identity of the nucleotide at a biallelic marker in CC a sample DNA sequence. The nucleotide sequences may be labelled and used CC primers by determining the identity of a nucleotide at a Region CC subjects. By determining the identity of a biallelic marker in a biological sample from single or multiple population an association between a genotype and a trait, a haplotype and constrained to determine a predisoposition to or early onset of schizophrenia or treatment and sorder or a beneficial response to or side effects related to treatment against schizophrenia or bipolar disorder.

Sequence 3001 BP; 842 A; 608 C; 584 G; 966 T; 1 other;

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밁
                                    Matches
                                                  Query Match
427 AGAGCTGCCCAAACTGCTTT 408
             1 agagatgcccaaactgtttt 20
                                           Local
                                  18;
                                         Similarity
                                 Conservative
                                      84.0%;
                                0,
                                              Score 16.8;
                                       Pred. No.
                             Mismatches
                                      61;
                                              DB 21;
                             2;
                                              Length 3001;
                             Indels
                             0;
                            Gaps
                           0;
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XX	RESULT 8 AAL03245/c ID AAL03245 standard; DNA; 9821 BP.  XX AC AAL03245; XX DT 21-NOV-2001 (first entry) XX DE Human reproductive system related antigen DNA SEQ ID NO: 5933.  XX XX KW cancer; gene therapy; ds. XX OS Homo sapiens. XX PN W0200155320-A2.
PR 29-SEP-2000; 2000US-0236369. PR 29-SEP-2000; 2000US-0236370. PR 02-CCT-2000; 2000US-0236370. PR 02-CCT-2000; 2000US-0237039. PR 02-CCT-2000; 2000US-0237039. PR 02-CCT-2000; 2000US-0237039. PR 02-CCT-2000; 2000US-0237040. PR 02-CCT-2000; 2000US-0241786. PR 13-CCT-2000; 2000US-0241786. PR 20-CCT-2000; 2000US-0241808. PR 20-CCT-2000; 2000US-0241808. PR 20-CCT-2000; 2000US-0244617. PR 01-NOV-2000; 2000US-0244617. PR 01-NOV-2000; 2000US-0246474. PR 08-NOV-2000; 2000US-0246476. PR 08-NOV-2000; 2000US-0246477. PR 08-NOV-2000; 2000US-0246476. PR 08-NOV-2000; 2000US-0246476. PR 08-NOV-2000; 2000US-0246478. PR 08-NOV-2000; 2000US-0246523. PR 08-NOV-2000; 2000US-0246523. PR 08-NOV-2000; 2000US-0246524. PR 08-NOV-2000; 2000US-0246526. PR 17-NOV-2000; 2000US-0246527. PR 18-NOV-2000; 2000US-0246528. PR 18-NOV-2000; 2000US-0246511. PR 17-NOV-2000; 2000US-0249211. PR 17-NOV-2000; 2000US-0249213. PR 17-NOV-2000; 2000US-0249213. PR 17-NOV-2000; 2000US-0249213. PR 17-NOV-2000; 2000US-0249213. PR 17-NOV-2000; 2000US-0249213	14-SEP-2000; 2000U 21-SEP-2000; 2000U

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RESULT 9
AAL03246/c
ID AAL032
XX AAL032
XX AAL032
XX DT 21-NOV
XX Human;
KW Human;
KW Cancer
XX Homo s
XX Homo s
YX HOZO01
XX IT-JAN
XX IT-JAN
PR 04-FEE
PR 24-FEE
PR 24-FEE
PR 02-MAI
PR 16-MAI
PR 16-MAI
PR 17-MAI
PR 19-MAI
PR 
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                         31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
102-MAR-2000;
11-6-MAR-2000;
11-6-MAR-2000;
11-6-AFR-2000;
11-AFR-2000;
11-MAY-2000;
07-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                     17-JAN-2001;
                                                                                                                                                                                                                                                                                           02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                            Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human reproductive system related antigen DNA SEQ ID NO: 5934.
                                                                                                                                                                                                                                                                                                                               W0200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL03246 standard; DNA; 9824 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL03246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2800 AGAGCTGCCCAAACTGCTTT 2781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9821 BP; 3056 A; 1735 C; 1689 G; 3341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 5933; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-465570/50.
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                     2000US-0186628
2000US-0184664
2000US-0186350
2000US-0189874
2000US-0190076
2000US-0198123
2000US-0295515
2000US-020467
2000US-0214886
2000US-0214886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.0%;
ilarity 90.0%;
Conservative
                                                                                                                                                                                                                                                   2001WO-US01339
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                                                                                                                                                                                                                 2000US-0179065
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; 2000US-0251988.
; 2000US-0256719.
; 2000US-0251479.
; 2000US-0251856.
; 2000US-0251868.
; 2000US-0251869.
; 2000US-0251989.
; 2000US-0251990.
; 2000US-0254097.
; 2000US-0254097.
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Pred. No. 74;
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         23-AUG-2000
30-AUG-2000
31-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
05-SEP-2000
05-SEP-2000
06-SEP-2000
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17-SEP-2000
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21-SEP-2000
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2000US-0239935.
2000US-0239937.
2000US-0240960.
2000US-0241221.
2000US-0241785.
2000US-0241787.
                                                                                                                                 2000US-0237038.
2000US-0237039.
2000US-0237040.
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2000US-0234223
2000US-0234274
2000US-0234997
2000US-02354998
2000US-0235834
2000US-0235834
2000US-0236367
2000US-0236367
2000US-0236368
2000US-0236368
2000US-0236368
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2000US-0232401.
2000US-0233063.
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2000US-0229513
2000US-0230437
2000US-0230438
2000US-0231242
2000US-0231243
2000US-0231243
2000US-02312413
2000US-0231414
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2000US-0232398.
2000US-0232399.
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2000US-0232081.
2000US-0231968.
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2000US-0216880.
2000US-0217496.
2000US-0217496.
2000US-0220964.
2000US-022964518.
2000US-0224518.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225276.
2000US-0225276.
2000US-0225277.
2000US-0225277.
2000US-0225277.
2000US-0225275.
2000US-0225775.
2000US-0225775.
2000US-0225775.
2000US-0225775.
2000US-0225775.
2000US-0225775.
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2000US-0237037.
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2000US-0229287.
2000US-0229343.
2000US-0229344.
2000US-0229345.
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2000US-0227182.
2000US-0227009.
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20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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2000US-0241809.
2000US-0241826.
2000US-0244617.
2000US-0246474.
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2000US-0246476.
2000US-0246477.
                                                                                                       Barash SC,
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2000US - 0249208.

2000US - 0249209.

2000US - 0249210.

2000US - 0249211.

2000US - 0249213.
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2000US-0246611.
2000US-0246613.
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2000US-0246523.
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2000US-0246532.
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2000US-0246526.
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2000US-0249216.
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2000US-0250160.
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                                                                                                                                                2000US-0251990.
                                                                                                                                                       2000US-0251989
                                                                                                                                                                           2000US-0251856
                                                                                                                                                                                         25671
                                                                                                       Ruben SM;
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WPI; 2001-465570/50.

is used in preventing, treating or ameliorating a medical condition Isolated nucleic acid molecule encoding a reproductive system antigen

Disclosure; SEQ ID NO 5934; 1297pp + Sequence Listing; English.

The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.

Sequence 9824 BP; 3057 A; 1735 C; 1689 G; 3343 T; 0 other;

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7383 agaaatgcacaaactgtttt 7402

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Best Local Similarity
                                                             Query Match
Best Local :
                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2800 AGAGCTGCCCAAACTGCTTT 2781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX13026;
                                                                                                                                                               A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based primary nucleotide sequences, also known as contigs. The computer-based primary nucleotide sequences, also known as contigs. The computer based for commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus faecalis; contig; detection; Enterococcal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecalis genome contig SEQ ID NO:89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and focuse in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9850555-A2
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 596-606; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-045171/04.
                                                                                                                                                                                                                                                                                                                                                                                                                          infection.
                                                                                                                     Sequence 20072 BP; 5846 A; 4288 C; 3266 G; 6628 T; 44 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 agagatgcccaaactgtttt 20
|||| |||||||||||||
1 agagatgcccaaactgtttt 20
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                                                              Similarity
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                                                Conservative
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97US-0044031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0046655
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90.0%;
                                                              90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunsch CA;
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Pred. No. 74;
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                                                                  Pred. No.
                                                                             Score 16.8;
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                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                  20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9824;
                                                                                  Length 20072;
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RESULT 11

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ZXXXXX
ZXXXXX
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                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                   The invention relates to a family of human genes referred to as the CC DAZ gene family, and to a functional DAZ homologue, DAZH. Members of the CC DAX gene family are clustered in the same region of the Y chromosome. CC In particular, the invention relates to an isolated DAZ gene (AAZ9249) present in interval 6D and/or 6E of the distal portion of Yq, mutations (CC In which are associated with reduced sperm count. The DAZH gene CC (AAZ92580) is located on chromosome 3; however, the entire DAZ gene CC (In which are sequences may be used as a source of primers and probes for uncledtide sequences may be used as a source of primers and probes for CC or deletion of the DAZ gene. They are also used as human chromosome Y reduced sperm count associated with alteration CC markers. Functional DAZ genes can be used in gene therapy for treating CC reduced sperm counts. Sequence AAZ9249 represents human DAZ cDNA, and CC aAZ92491-Z92492 are partial DNA sequences of DAZ gene family members.
                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ92583
                                                                                                                                                            22516 agagattgccaaactgtttt 22535
Pyrococcus abyssi genomic fragment #5
                                   29-OCT-2001
                                                                AAH41226;
                                                                                    AAH41226 standard; DNA; 349980 BP
                                                                                                                                                                                                                                                                                     Sequence 43795 BP; 12175 A; 8166 C; 8183 G; 15271 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Fig 11A-L; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid, useful for diagnosis and treatment of reduced sperm count, is derived from the human DAZ or DAZH genes - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-181393/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
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31-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAZ gene; chromosome vq; male infertility; sperm count; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6020476-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human DAZ genomic sequence, SEQ ID NO:101.
                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-2000 (first entry)
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                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                        Conservative
                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reeve MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0690734.
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                                                                                                                                                                                                                                    84.0%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                    Score 16.8;
Pred. No. 9
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page DC,
                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                               DB 21;
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                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                             Length 43795;
                                                                                                                                                                                                                  Indels
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AC XXX
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                  53995 aaagatacccaaactgtttt 54014
           Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque;
        comato; monkey;
                                                                          Human EST-derived coding sequence SEQ ID NO: 980.
                                                                                                                                                  12-OCT-2001
                                                                                                                                                                                                              ААН99123;
                                                                                                                                                                                                                                                        AAH99123 standard; cDNA; 396 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the genomic sequence of Pyrococcus abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. abyssi. The 5' end of this sequence overlaps with the 3' end of AAH41225 and the 3' end of this sequence overlaps with the 5' end of AAH41277. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 349980 BP; 98084 A; 80447 C; 77665 G; 93784 T; 0 other:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 511-606; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleotide sequences isolated from Pyrococcus abyssi encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-126236/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CNRS ) CNRS CENT NAT RECH SCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 agagatgcccaaactgtttt 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                         (first entry)
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Weissenbach J,
dog; sea urchin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99FR-0005034.
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/*tag= b
/note= "This sequence overlaps with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH41225"
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1..49980
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/note= "This sequence overlaps with the 3/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.8; DB 22
Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dietrich J, W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 349980;
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                    horse;
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expressed sequence tag; EST;

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SOXX CCCCCCCCX PXX PTTXX PTXX PTX
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AAF63808,
ID AAF6
PDD PNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the invention.
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 766; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibodies and research use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 396 BP; 80 A; 115 C; 86 G; 115 T; 0 other;
                                                                                                                                                                                                                                  Human; immunosuppressive; antiarthritic; antirhedmatic; nootropic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; autoimmune disease; hyperproliferative disorder; cancer; cardiovascular disorder; cerebrovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF63808 standard; cDNA; 1157 BP
                                                                                                                                                                                  secreted protein; ss.
                                                                                                                                                                                                               nervous system disorder; ocular disorder; chemotaxis; food additive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 agaaatgcccaaactgtt 139
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                                                                                                                                                                                                                                                                                                                                                                                                                           secreted protein gene 20 SEQ ID NO:30.
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Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ou P, Qian XB, Wang Z,
Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.0%;
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70;
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WO200077021-A1

21-DEC-2000

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RESULT 15
AAZ49395/c
ID AAZ493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which encode human secreted proteins AAB75280 - AAB75287. Included in the convention are protein sequences AAB75288 - AAB75287. Included in the convention are protein sequences AAB75288 - AAB75241 which are fragments of the secreted proteins and amino acid sequences with which these conventions and the activities of the activities of the proteins and the activities of the proteins and the proteins and the activities of the activities of the proteins and conventions are polynucleotides and the activities of the proteins and antisponists in their agonists and antisponists may be useful for treating preventing and diagnosing diseases and disorders such as autoimmune diseases e.g. rheumatoid arrthritis, hyperproliferative disorders c.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, c.g. antisponists and fungi and cular disorders c.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, c.g. antisponists and fungi and cular disorders c.g. cerebral ischaemia, c.g. corneal infection. The polypeptides can also be used to ald wound c.g. corneal infection. The polypeptides can also be used to ald wound e.g. corneal infection. The polypeptides can also be used to ald wound c.g. culture of primary tissues, to regenerate tissues and in chemotaxis. The c.g. culture of primary tissues, to regenerate tissues and in chemotaxis. The c.g. culture of cornease storage capabilities. Included in the invention are oligonucleotides AAF63780 - AAF63780 and peptide AAB75239 which are used in the identification and characterisation of the DNA and protein
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    KKKKKX DX DX ACX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecules encoding human secreted proteins, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 451; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing, treating or ameliorating preventing, treating or ameliorating preventing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences of the invention.
                    Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; pancreatic cancer; ovarian cancer; tumour antigen; immunisation; immune response;
                                                                                                                                                                                                                  AAZ49395;
                                                                                                                                                                                                                                                             AAZ49395 standard; cDNA; 1193 BP
                                                                                                                             Human STRAP-1 cDNA
                                                                                                                                                                           14-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                  |||| |||||||||| 1||
138 GAGAAGCCCAAACTGCTTT 120
cellular; humoral; anticancer vaccine; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             2 gagatgcccaaactgtttt 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.0%;
89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.8; DB 22
Pred. No. 1.7e+02;
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           detection; diagnosis,
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cype IIIa membrane protein and is expressed predominantly in prostate cells in normal human tissues. Structurally, STRAP-1 is thought to be a cid protein characterised by six transmembrane domains and in protein characterised by six transmembrane domains and comminantly in prostate carid protein characterised by six transmembrane domains and comminantly in protein in comminantly in protein in comminantly in comminantly in protein in comminantly comminantly in comminantly comminantly in comminant comminantly in comminant comminantly in comminant comminantly in comminant comminant comminantly in comminant comminantly in comminant comminant comminantly in comminant comminant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents cDNA encoding a novel human protein, STRAP-1 (serpentine transmembrane antigen of the prostate). STRAP-1 is the prototype member of the STRAP family of proteins (AAY58194-Y58197) which exhibit a high degree of structural conservation, but which show no significant structural homology to known human proteins. The STRAP-1 gene has been localised to chromosome 7p22. STRAP-1 is thought to be a
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P-PSDB; AAY58194.
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(HUBE/) HUBERT R S.
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drug targetting; recombinant protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) LEONG K.
) RAITANO A B.
SAFFRAN D C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0087520.
98US-0091183.
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antigen of the prostate)"
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Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 other:

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В
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                                           Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                              Matches
564 GAGAAGCCCAAACTGCTTT 546
          2 gagatgcccaaactgtttt 20
                                          Conservative
                                          0; Mismatches
                                                      Score 15.8; DB 21;
Pred. No. 1.7e+02;
                                     8; LL
. 1.7e+02;
2;
                                                              Length 1193;
                                          Indels
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                                      Gaps
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Search completed: September 7, 2002, 18:39:44 Job time: 29878 sec

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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    Result
No.
                                                     pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
     Score
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    Query
Match Length DB
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Gapop 10.0 , Gapext 1.0
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                                    SUMMARIES
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       Description
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AX026100
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DEFINITION
ACCESSION
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                                                   FEATURES
                                                                                         AUTHORS
TITLE
                                                                      JOURNAL
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 1984779-C 12 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
                                                                                                                                                                                AX026100 20 bp
Sequence 12 from Patent DE19847779.
AX026100
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 20)
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134686
14686
166906
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                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                  Location/Qualifiers
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661
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AX026106
AX026114
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AF363304
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AC110307
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AE001670 Chlamydia
AE002255 Chlamydop
AC015202 Drosophil
AL591593 Zebrafish
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AX026106 Sequence
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X87625 H.sapiens C
AX026092 Sequence
AX026089 Sequence
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AP004461 Oryza sat
ACO91962 Homo sapi
AL671173 Mus muscu
AL627345 Mus muscu
AX026101 Sequence
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Z68871 Human DNA s
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X79942 Human Papil
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DEFINITION
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AX026114
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Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 26 03-FEB-2000;

DEUTSCHES KREBSFORSCH (DE)
                                                                                                                                                                                                                                                                                                                             AX026114 40 bp
Sequence 26 from Patent DE19847779.
AX026114
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Sequence 18 from Patent DE19847779,
AX026106
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Mueller-Schilling, M., Krammer, P. and Oren, M.
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 282); Minimum (base); Louis (b
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Sequence 4 from Patent DE19847779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Rudert, F.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96069539
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1 (bases 1 to 2344)
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/map="q24.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3212 bp
Sequence 1 from Patent DE19847779.
AX026089
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mueller-Schilling,M., Krammer,P. and Oren,M. Novel receptor dna useful for identifying apoptosis-mc substances potentially useful for cancer chemotherapy patent: DE 19847779-C 1 03-FEB-2000;
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1 (bases 1 to 3212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                    AL157394
                                                                                                                                                                                                                  Human DNA sequence from clone
             Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 187313)
                                                                                                                          Homo sapiens
                                                                                                                                                                       AL157394.15 GI:15384622
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                                                             Blakey,S
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                                            Submission
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
784 c 809 g 841
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clonerequest@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; DB 100.0%; Pred. No. 1.4;
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                                                          REFERENCE
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following assembly was confirmed by restriction digest. The following in the feature table with their source databases: Em., EMBL; Sw:, in the feature table with their source databases:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RP11-399019 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                sequence.
AL513364
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                                                                                                                                                                                                                                                                                                                 Human DNA sequence from clone RP11-480N10 on chromosome 1, complete
Direct Submission
                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 74951)
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                              Almeida, J
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                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Sequence confirmed by AC015461 sequenced by WIBR." 55669~\mathrm{a} 36398~\mathrm{c} 36888~\mathrm{g} 58358~\mathrm{t}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is the entire insert of clone RP11-399019 The true end of clone RP11-496H23 is at 166408 in this sequence. The right end of clone RP11-304I5 is at 18704 in this sequence. Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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/clone_lib="RPCI-11.2"
100119 . 100156
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                            74951 bp
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humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Nov 16, 2001 this sequence version replaced gi:16944088.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
http://www.sanger.au/Voredenters/
                                Homo sapiens chromosome 1 clone RP4-722L13 map p22.3-31.2, ***
AL365355
                                                                                                              AL365355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone RP11-480N10 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-480N10 is at 74951 in this sequence. The true left end of clone RP11-77G8 is at 42605 in this sequence. The true right end of clone RP11-541J2 is at 2000 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1 RP11-480N10 1s from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Single clone region. Assembly consistent with restriction digest data."
14184 c 13984 g 21266 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be approximately 300bp by complement(48432. .48507)
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/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Tandem repeat. Forced join. Gap size estimated to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP11-480N10"
/clone_lib="RPCI-11.2"
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95.0%;
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Pred. No. 18
                                                                                                        90478 bp
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                                                                                                                                                                      misc_feature
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21294 21393: gap of 100 bp

21394 37557: contig of 16164 bp in length

37558 37657: gap of 100 bp

37658 54929: contig of 17272 bp in length

54930 55029: gap of 100 bp

54930 55029: gap of 100 bp

55030 62839: contig of 7810 bp in length

62840 62939: gap of 100 bp

62840 62939: gap of 100 bp

62840 74511: contig of 7810 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 87417 bases at least Q30 Consensus quality: 88119 bases at least Q20 Insert size: 89678; sum-of-contigs Insert size: 92914; 9.4% error; agarose-fp Quality coverage: 4.75x in Q20 bases; sum-of-contigs Quality coverage: 4.78x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5 sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator Big Dye; 55% of reads Chemistry: Dye-terminator ET-amersham; 44% of reads Consensus quality: 86233 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: dJ722L13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Sanger Centre
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On Aug 12, 2000 this sequence version replaced gi:9187428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pavitt, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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62940 74511; contig of 11572 bp in length
74512 74611; gap of 100 bp
74612 83633; contig of 9022 bp in length
83634 83733; gap of 100 bp
83734 90478; contig of 6745 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12390 12489: contig of 12389 bp in length
12490 17235: contig of 4746 bp in length
17236 17335: gap of 100 bp
                    /note="assembly_fragment:00528
fragment_chain:1"
                                                                                                   /note="assembly_fragment:00957
fragment_chain:1"
                                                                                                                                                                                                                 /map="p22.3-31.2"
/clone="RP4-722L13"
                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                          /clone_lib="RPCI-4"
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                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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    Summary Statistics

    Project Information

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                                                                                                    COMMENT
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                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C., Lander, E!, Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F.; Boguslavkiy, L., Anderson, S., Baldwin, J., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Fernestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Fenestor, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., McBen, P., McGurk, A., McKernan, K., McDheeters, R., McIdrim, J., McEwan, P., McGurk, A., McKernan, K., McDheeters, R., McIdrim, J., McBwan, P., McGurk, A., Mranda, C., Mlenga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Survers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Pollara, M., Mison, J., Ve, M., Mison, J., Zimmer, A. and Pollara, M., Mison, J., Zimmer, A. and Pollara, M., Santos, R., Schauer, A., and Pollara, M., Mison, J., Zimmer, A. and Pollara, M., Mison, J., Lander, S., Lander, A., Lander, A., Mison, M., Lander, A., Lander, A., Mison, J., Lander, A., Lander, A., La
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                               Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 14, 2000 this sequence version replaced gi:7108032.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                         Direct Submission
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fragment_chain:1"
21394._.37557
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83734. .90478
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pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106040 106139; gap of 106140 123134; cont
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24125 30616: contig of 6492 bp in length
30617 30716: gap of 100 bp
30717 35830: contig of 5114 bp in length
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4121 4220: gap of 100 bp
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6094 6100
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2239; contig of 1122 bp in length
2230 2329; gap of 100 bp
2330 4120; contid of 170
4121 4220.
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/clone="RP11-23I23"
/note="assembly_fragment"
                                                                           /note="assembly_fragment"
                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                          /clone_lib="RPCI-11 Human Male BAC"
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123134; contig of 16995 bp in length
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91285: contig of 12558 bp in length
385: gap of 100 bp
106039: contig of 14654 bp in length
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45340: contig of 9410 bp in length
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COMMENT
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Best Local Similarity 95.0%;
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                          Direct Submission
Submitted (16-NOV-2001) Genome Center, University of Washington, Sox 352145, Seattle, WA 98195, USA
On Nov 16, 2001 this sequence version replaced gi:12331033.
                                                                                                       Kaul,
                                                                                                                                                                                                                                                                    Homo sapiens chromosome I clone RP11-193H16, WORKING DRAFT SEQUENCE, 9 unordered pieces.
AC099561 AL356153
AC099561.1 GI:16945998
                                                                                                                                                     1 (bases 1 to 181497)
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
                                                                                                                                                Direct Submission
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                               Homo sapiens
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                                                                                                               (bases 1 to 181497)
Center: University of Washington Genome Center
                                                                                            ,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
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/note="assembly_fragment"
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31221 c 31549 g 49758 t
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123235 .140131
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91386. .106039
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30717. .35830
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12757. .19311
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Pred. No. 20;
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BASE COUNT
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              58138 a
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Sequencing vector: plasmid; 10% of reads
Chemistry: Dye-terminator E1; 73% of reads
Chemistry: Dye-terminator B1g Dye; 27% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 176140 bases at least Q40
Consensus quality: 179264 bases at least Q30
Consensus quality: 179264 bases at least Q20
Insert size: 169266; 11.4% error; agarose-fp
Quality coverage: 8.9x in Q20 bases; sum-of-contigs
Quality coverage: 8.4x in Q20 bases; sum-of-contigs
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Drafting Center: SC
-----Project Information
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Center clone name: RP11-193H16 (sc0121)
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2456
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/note="assembly_name:Contig106"
109809. 181497
/note="assembly_name:Contig107"
1 34626 c 32770 g 55026 t
                                                                                                  /note≈"assembly_name:Contig105"
52282. .109708
                                                                                                                                                                /note="assembly_name:Contig104"
                                                                                                                                                                                                            /note="assembly_name:Contig103"
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2456. .4495
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                             note="assembly_name:Contig102"
                                                                                                                                                                                                                                                                                                          note="assembly_name:Contig101"
                                                                                                                                                                                                                                                                                                                                                                  /note='
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26889: contig of 9618 bp in length
26989: gap of unknown length
62181: contig of 35192 bp in length
62281: gap of unknown length
109708: contig of 47427 bp in length
109808: gap of unknown length
181497: contig of 71689 bp in length
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2455: gap of unknown length
4495: contig of 2040 bp in length
4595: gap of unknown length
7640: contig of 3045 bp in length
7740: gap of unknown length
12425: contig of 4685 bp in length
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1: contig of 4646 bp in length
    937 others
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ORIGIN

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission

Direct Submission

Submitted (11 NOV-2000) Lita Annenberg Hazen Genome Sequencing Submitted (11 NOV-2000) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA

On Feb 3, 2001 this sequence version replaced gi:11276152.

On Feb 3, 2001 this sequence Center Center Cold Spring Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC084744 236685 bp DNA linear HTC Mus musculus clone RP23-15A13, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 236685)

McCombie, W.R., Baker, J.P., Bahret, A., Bal, H., Balija, V.,

Dedhia, N.N., de la Bastide, M., Huang, E.N., King, L., Kirchoff, K.A.,

Miller, B., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R.,

Rodriguez, S., Santos, L., Shah, R.S., Spiegel, L.A., Toth, K., Vil, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 236685)
McCombie, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Genomic Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                    Center project name: RP23-15A13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                       Center clone name: RP23-15A13
                                                                                                                                                                                                                                                                                                                                                                                              Contact: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.cshl.org/genseq
                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: CSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory
                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence! It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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57894
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42141
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95.0%;
             119883:
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                                        110735:
                                                     110626:
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                                                                                              85541:
                                                                                                             85432:
                                                                                                                                                    58002:
                                                                                                                                     72097:
                     2: gap of unknown length
7: contig of 14095 bp in length
6: gap of unknown length
2: contig of 13226 bp in length
1: gap of unknown length
1: contig of 12550 bp in length
0: gap of unknown length
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5: contig of 12426 bp in length
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 gap of contig
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of 8849
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CE, 35 unordered
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AE001670/c
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                                                                                                                                 Conservative
                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
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57976 c 57568 g 58324 t
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191171: contig
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235387; contig of 1946 bp in length
235495: gap of unknown length
236685: contig of 1190 bp in length
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of 4228
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f unknown
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BCT 01-DEC-2000

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Gaps

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COMMENT

TITLE

TITLE

REFERENCE

AUTHORS

VERSION ACCESSION

KEYWORDS

Locus

Matches

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FEATURES
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1 (bases 1 to 16157)

Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R.W., Olinger, L., Grinwood, J., Davis, R.W. and Stephens, R.S.

Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydophila pneumoniae CWL029. Chlamydophila pneumoniae CWL029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="CPn0894"
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                                  SOURCE
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Best Local
      ORGANISM
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Chlamydophila pneumoniae AR39
Chlamydophila pneumoniae AR39
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AE002255.2 GI:8163532
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### PRILMGASEPPENIDLY IRSPGIFF PARAMONIGLE PLUMGOPGVERVEISSFOLA
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TOTELLANGNIGHT PLUMGOPGVERVEISSFOLANGNIGLE PLUMGOPGVERVEISSFOLANGN
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FDQFQSFKERGAYFKLLIREMQAVR"
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94.7%;
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Pred. No. 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 28 (6), 1397-1406 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumoniae AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medical Center Dr, Rockville, MD 20850, USA
On Jun 1, 2000 this sequence version replaced gi:7189881.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10684935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="conserved hypothetical protein; identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VHFQATTIGQREPKVYRSLGADSVCITGDESLTAMDGEFLLAKHFVETLAKHSSYYLL
PGNHDYYTLKSLAQQTFYTHFPNDQLQQNKVSFHKITDHWWLILLDCSCLNGWFSANG
VYHLAQISAIETFLLSLSPEENVIIANHYPLLSSQNPSHDLINNTHLQNVLKKYPKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="CP0969"
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/strain="AR39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1030. .1251)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="conserved hypothetical protein; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="synonym: Chlamydia pneumoniae AR39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:115711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1030. .1251)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFDAPLEIANEATWDCQKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYLHGHEHQAAVYNCADTSPSYILNSGSISLPTNSRFHVIDLYPEKYQVHTMILKNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MQEKPRHVHRIIHISDVHFHVLPVNPVHCFNKRLKGLLRKVFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIREIEKEERVETPQLFQAIAEKILEEGV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1295. .1867)
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                                                                                          NFLTGRVIERTYKSGESVETADIVERSMRLLYTDQEGATFMDDETFEQEVVFWEKLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CP0971"
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                                                                                                                                                                                                                                                                                                                                                             /note="similar to GB:U14003 SP:P33398 GB:X61676 PID:433670
                                                                                                                                                                                                                                                                                                                                                                                                /gene="CP0971"
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/note="similar to SP:P30958 GB:U00096 PID:1651547 PID:1651549 PID:1787357; identified by sequence
                                                                                                                                        /gene="CP0975"
7782. .11039
                                                                                             /gene="CP0975"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEIDGYDFHHIBEFESSIRGOERPYLVIAHTIIGHGSPKEGTNKAHGSPLGVEGTH
ETKOFWHLPEEKFEVPPAVKNFFAHKIQEDRKAQEQWLDEVRVWSKOFPELHBEFVAL
TSHKLPKNLESLVQSVEMPDSIAGRAASNKLIQVLVQHIPYLIGGSADKSSEDGTWIA
NEKVIHTYDESGRNIKYGVBEFGMATINNGLAYSQVFREPEGGTELVESDYMRNAIRK
ALSKLPVIYQFTHDSIFVGEDGPTHQPVEQLMSLRAIFGLYVIRPADANEVRGAWIAG
LKHTGPTVIVLSRAALPTLFAAHRPFEDGVGRGAYIVLKESGEKDYTLFATGSEVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"similar to GB:J01581 SP:P00957 PID:145220 GB:U00096 PID:1789048; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALSVAKELEHLDKÖVRVVSFPCWELFEAQDVDYKOSIVGGDLGIRVSIEAGSALGWYK
YIGSBGLAIAMDRFGYSGASDDVSEECGFTTEQILQRILSQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="CP0974"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDGCFMEGVSHEVCSFAGSLNLNNLVVIYDYNNVVLDGYLNEISVEDTKKRFEAYGWD
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RTPGHPEYGETVGVEATTGPLGOGLGNAVGMALSMKMLESRFNRPGHEIFNGKIYCLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="transketolase"
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PID:1788808; identified by sequence similarity; putative"
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Thttnirfweenkkfrkklyetkaqsaemecatlfaagyrrnlpigalllisdlplrk
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/gene="CP0973"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:1736646;
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                                                                                                                                                                                                              11039
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CDS gene

SOURCE

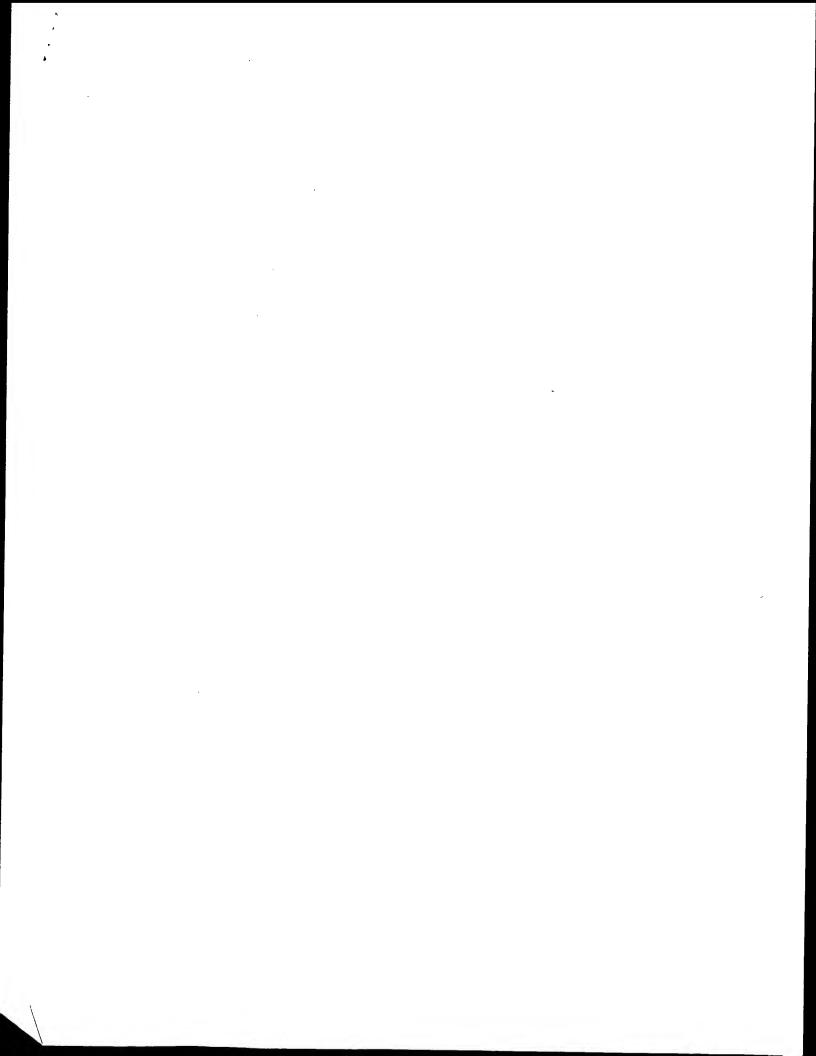
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                   AC015202
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Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
                           Adams, M. and Venter, J.C. Direct Submission
                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 20563)
                                                                                                                                        Drosophila melanogaster
                                                                                                                          Eukaryota;
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                                                                                                                                                              fruit fly.
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/protein_id="AAF38756.1"
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* This sequence will be replaced  * by the finished sequence as soon as it is available and  * the accession number will be preserved.  FEATURES  Location/Qualifiers	6416 a	Query Match 87.0%; Score 17.4; DB 2; Length 20563; Best Local Similarity 94.7%; Pred. No. 62; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy 1 agagatgcccaaactgttt 19 .   		Grganism-"Drosophila melanogaster"  /db_xref-"taxon:7227"  6416 a 4099 c 4148 g 5900 t  87.0%; Score 17.4; DB 2; Length 2056  11 Similarity 94.7%; Pred. No. 62;  18; Conservative 0; Mismatches 1; Indels  placed: September 7, 2002, 18:21:55  28814 sec
120563	Query Match  87.0%; Score 17.4; DB 2; Length 20563;  Best Local Similarity 94.7%; Pred. No. 62;  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps  1 agagatgcccaaactgttt 19  1	1 agagatgcccaaactgttt 			September 7, 2002, sc
120563 /organism="Drosophila melanogaster"/ /db_xref="taxon:7227" /db_xref="taxon:722	Query Match  Best Local Similarity 94.7%; Pred. No. 62; Length 20563;  Best Local Similarity 94.7%; Pred. No. 62; Length 20563;  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 1 agagatycccaaactyttt 19	1 agagatgcccaaactgttt 19	September 7, 2002, sc		
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      Homo sapiens genomic DNA, 21q region, clone: B2289H10 genomic survey sequence.
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AG019562
                                         AG019562
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Submitted (16-OCT-1999) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, RIKEN Genomic Sciences Center(GSC) c/o Kitasato
University; 1-15-1 Kitasato, Sagamihara 228-8555, Japan
(E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:042-778-9923,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T., Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1999) In press
2 (bases 1 to 488)
Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.,
Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
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""Amatches 33;
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                                                                                            Insert Length: 717 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 398.
                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 717 Std Error: 0.00
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                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zt08e01.s1 NCI_CGAP_GCB1 Homo
                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
AA279976
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Masahira Hattori, RIKEN Genomic Sciences Center(GSC) c/o Kitasato
University; 1-15-1 Kitasato, Sagamihara 228-8555, Japan
(E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:042-778-9923,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax:042-778-9924)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y Homo sapiens genomic DNA, chromosome 21g Published Only in DataBase (1999) In press 2 (bases 1 to 756)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                      ocation/Qualifiers
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/map="21g"
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Local Similarity 64.2%;
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HS_2226_A2_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2226 Col=2 Row+G, DNA sequence.
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1 (bases 1 to 421)

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                         401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                        High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                             scanning the human genome
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                                                                                                                                                                            High quality sequence stop: 421.
                                                                                                                                                                                                  Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
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/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                  /clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                         ocation/Qualifiers

 Mismatches

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Pred. No. 0.096;
0; Mismatches 34;
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                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 actaaccatctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 33.5%;
Local Similarity 63.2%;
les 60; Conservative
                                      180 AAAAGCCCAGACTTTGAAGCCAGACTGCTTAGGTTCAAATCCTGGCTCTGCCAGTTATTA 239
                                                                         6
85 actaaccatctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-094G15.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (TSUTUMI-KU, YOKhohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, TSUTUMI-KU, YOKhohama, Kanagawa 230-0045, Japan (E-mail:chimpbes/gSc.riken.go.jp, URL:http://hgp.gSc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-603-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes DNA, clone: PTB-094G15.F, genomic survey sequence. AG093829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG093829.1 GI:16645631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 698)
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                                                                                                                                                                                                                                     197 a
                                                                                                                                                                                                                                                                                                                                                                                                         Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing: -21M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tracking errors.
                                                                                                                                                                                                                                   /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
165 c 134 g 198 t 4 others
                                                                                                                                                                                                                                                                                                                                                                         1. .698
                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                  /clone="PTB-094G15.F"
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9598
                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                       32.5%; Score 39; DB . 63.2%; Pred. No. 0.3;
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                                                                                                                         0; Mismatches 35; Indels
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                                                                                                                                                                DB 12; Length 698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                             133 TGGCTCTGTTACTTATAAGCTCTGCAACCTCGGGCAGATTACCTAAGTCAGTTT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                         67 tgactctgctatttattaactaaccatctttgccaatgttgcttaagctttttt 120
                                                                                                                                              73 ATGGAGGGACAGAGATGGTAAAACATGGTCTTGGAAGCCAGACCGTCTGGGTTTGAATCC 132
                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                          7 aagggggtatggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcc 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
        AQ240694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 530.
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 530)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T. Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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AQ708262
HS_5571_A1_F11_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1147 Col=21 Row-K, DNA sequence.
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                                                                                                                                                                                                                                                                                                                             165
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                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="Plate=1147 Col=21 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
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                                                                                                                                                                                                                                    32.3%;
58.8%;
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                                                                                                                                                                                                                                Score 38.8; DB 12; Length 530; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                      104 g
 691 bp
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   DNA
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linear
GSS 30-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 ATGCAGAATTAAAAGTATAGGCACTGGAGCCAGATTCACTCAGTTTTAAATGCAACTCTT 71
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                                                                                                                                                                                                                                                                                                                                                                                               70 CAATTTCTTAGATAAATGACTTTGTCCAAGTTTCTTAAGCTT 29
                                                                                                                                                                                                                                                                                                                                                                                                                      75 ctatttattaactaaccatctttgccaatgttgcttaagctt 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 atggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctg 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 367)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                           367 bp mRNA linear EST 21-APR-1997 EST89574 Small intestine I Homo sapiens cDNA 5' end, mRNA sequence. AA376998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                        AA376998.1 GI:2029388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
Other_GSSs: CIT-HSP-2386K22.TR.1
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a 99 c
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/note="Yector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="2386K22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="CIT-HSP"
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Pred. No. 0.58;
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                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                            EST 21-APR-1997
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COMMENT
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AQ498448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter, J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: arkerlav@tigr.org
For clone availability, additional sequence and expression for clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                             AQ498448 437 bp DNA linear GSS 28-APR-
HS_5088_B1_F12_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=664 Col=23 Row=L, DNA sequence.
                                                                                                                              1 (bases 1 to 437)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                         Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                         Homo sapiens
99380589
                                                  scanning the
                                                                                                                                                                                                                                                                                                                                                           AQ498448.1 GI:4698571
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                    Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: small intestine; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

s 64 g 134 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="ATCC (inhost):181474"
/db_xref="taxon:9606"
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                                                       human
                                                       genome
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Pred. No. 0.79;
0; Mismatches 16;
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FEATURES
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                                                                                                                                                                                       TITLE
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 664
                                                                                                                                                                                                                                                                                                                                                                                                                                        CIT-HSP-2343H11.TF CIT-HSP Homo sapiens genomic clone 2343H11, DNA
                                                                                                                                                                                                   Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ054706
                                                                                                                              Unpublished (1998)
Other_GSSs: CIT-HSP-2343H11.TR
                                                                                                                                                                                   Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                   AQ054706.1
              Tel: 301 838 0200 Fax: 301 838 0208
                                                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                            Contact: Mark Adams
                                                                                                                                                                     Building
                                                  9712 Medical Center Dr., Rockville,
Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
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1. .437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="Plate=664 Col=23 Row=L"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.2%;
74.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                605 bp
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                                                               MD 20850, USA
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 actaaccatctttgccaatgttgcttaagctttttt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                         High
                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (Plate: 0400 row: K column: 14
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                        Class: plasmid ends
                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 686)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1M0400K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC1M0400K14 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ590942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end search
                                                                                                                                                   quality sequence stop: 686.
                                                                                                                                                                                                                                                                                                                                 308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                             USA
/db_xref="taxon:10090"
/clone="UUGC1M0400K14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                             Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
### 102 c 104 g 178 t
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/sex="Male"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                            Std Error: 0.00
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FEATURES
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AQ603697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                           High quality sequence stop: 482.
                                                                                                                                               Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2126 row: C column: 9
                                                                                              Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                               401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                         High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                    scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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482 bp DNA linear GSS 10-JUN-1998
HS_2126_A1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2126 Col=9 Row=C, DNA sequence.
AQ603697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ603697.1 GI:5063691
                                                                                                                                                                                                                                              (206) 616-3618
(206) 616-3887
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                                                                                                                                                                                                                                                                                                                                                                                                   Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonucleotides were adaptored DNA was purified and size-selected for a 9.5 to electrophoresis. Vector DNA was prepared from a derivative of pWD42 (91|4733114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA
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Pred. No. 1.5;
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                                            Query Match
         Matches
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29.8%;
Local Similarity 61.1%;
les 58; Conserva+1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGTGTGACCTTGGGCAAGTTACTTAACCTCTCT 182
                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-AUG-2001) Asao Fujiyama, The Unstitute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AG040377.1 GI:16569102
GSS; GSS (genome survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AG040377

640 bp DNA linear GSS 01-NOV-200
Pan troglodytes DNA, clone: PTB-017M07.F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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troglodytes male lymphoblast DNA, clone lib:PTB Chimpanzee Male Library clone:PTB-017M07.F.
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R.Site 2
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E-Coli DH10B"
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/clone="Plate=2126 Col=9 Row=C"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                     /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
143 c 125 g 180 t
                                                                                                                                                                                                              /organism≖"Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                           /sex="male"
                                                                                                                                                                                             /clone="PTB-017M07.F"
                                                                                                                                                                                                                                                                 Location/Qualifiers
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                           Score 35.8; DB 12; Pred. No. 2.5;
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                                                                            559 AAGAACACAGCCTCTGGAACCAGATTGCCTGAGCTCAAATCCTGTGTCTGCCACTTATTG 500
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                                                                                                    GCTGTGTAATCTGGGCAAAGTTACTTAGAATCTCT 465
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HS_3100_A1_E01_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3100 Col=1 Row=I, DNA sequence.
AQ889826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3100 row: I column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-5618
Fax: (206) 616-2887
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Location/Qualifiers
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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Class: BAC ends
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Similarity 61.1%;
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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/db_xref="taxon:9606"
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Search completed: September Job time: 16183 sec

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Post-processing: Minimum Match 0%
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1: /cgn2_6/ptodata/2/pna/U

2: /cgn2_6/ptodata/2/pna/U

3: /cgn2_6/ptodata/2/pna/U

4: /cgn2_6/ptodata/2/pna/U

5: /cgn2_6/ptodata/2/pna/U

6: /cgn2_6/ptodata/2/pna/U

7: /cgn2_6/ptodata/2/pna/U

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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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                      8, 2002, 01:09:18; Search time 1826.34 Seconds (without alignments)
200.099 Million cell updates/sec
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         US-10-035-832-1262
US-10-027-632-281585
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US-09-345-882-1
US-10-027-632-152436
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US-10-027-632-152438
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57014, A
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14451, A
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28.2	28.2	28.2	28.2	28.2	28.3	28.5	28.5	28.5	28.5	28.7	28.7	28.7	28.7	28.8	28.8	28.8	0		29.0
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US-10-027-632-30428	US-10-027-632-190490	US-10-027-632-190489	US-10-027-632-190488	US-10-027-632-185527	US-10-027-632-277529	US-10-105-299-14994	US-10-126-103-273	US-10-027-632-177	US-10-198-846-12340	PCT-US02-25766-1885	US-10-027-632-102248	US-10-027-632-102247	US-10-137-757-619	US-10-027-632-323053	Q8-09-918-995-10146	US-09-918-995-12552	PCT-US02-21669-3	US-10-212-054-2144	US-10-206-664-2409
Sequence 30428, A	190490,					Sequence 14994, A	Sequence 2/3, App	1//,	1234		Sequence 102248,							2 T 4	2409,

## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: Patentin version 3.1
SEQ ID NO 1262
LENGTH: 45121
US-10-027-632-281585/c

Sequence 281385, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
ITITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITITLE OF INVENTION: Polymorphisms in the Human Genome
ITILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
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GENERAL INFORMATION:
APPLICANT: MORTLS, David
APPLICANT: Mogelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
FILE REFERENCE: A-71249/RMS/DCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-10-035-832-1262
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Best Local Similarity
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 Mismatches

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APPLICATION NUMBER: US 60/193,483 FILING DATE: 2000-03-29 APPLICATION NUMBER: US 60/198,676

FILING DATE:

2000-04-20

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; LENGTH: 633
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281585
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SEQ ID NO 129548
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                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                  ORGANISM: Human
                                                                                                                                                                                                      TYPE: DNA
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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23 gaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgctatttat 82
                                                                                    Local Similarity
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FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
                                                              58; Conservative
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                                                                                Score 36.4; DB Pred. No. 0.25;
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                                                              Mismatches
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT ETLING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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LENGTH: 637
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Best Local :
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR ETLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR EILING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.2%;
Local Similarity 59.0%;
les 62; Conservation
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FILING DATE: 1999-11-23
                        APPLICATION NUMBER: US 60/167,363
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; ORGANISM: Human
US-10-027-632-57014
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RESULT
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24 APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23 APPLICATION NUMBER: US 60/156,358
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APPLICATION NUMBER: US 60/146,002
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; LENGTH: 604
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-4265
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Best Local :
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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CURRENT FILING DATE: 2002-04-30
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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                                            PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                    PRIOR APPLICATION NUMBER: US 60/146,002
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FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
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NO 4266
TH: 604
                                                                                                                                                FILING DATE: 1999-09-28
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US-10-027-632-265257

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US-10-125-540-595/c
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; ORGANISM: Human
US-10-027-632-4266
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 595
LENGTH: 13046
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Best Local Similarity
                                                                                                     PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                  FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ14C1
                                                                        PRIOR
                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.
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ORGANISM: Homo sapiens
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                               APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23
              APPLICATION NUMBER: US 60/156,358
                                                                                   APPLICATION NUMBER: US 60/185,218
FILING DATE:
                                                                    FILING DATE: 2000-02-24
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Pred. No. 0.7;
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Pred. No. 0.34;
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APPLICANT: BOUGUETET, Lydie
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patent.pm
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1,
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 265257
LENGTH: 657
TYPE: DNA
ORGANISM: Human
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PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
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                                                         LOCATION: 97152
OTHER INFORMATION:
                                                                        NAME/KEY: allele LOCATION: 97152
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NAME/KEY: allele
LOCATION: 97122
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                  NAME/KEY: allele
LOCATION: 99098
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LOCATION: 93714
OTHER INFORMATION:
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LOCATION: 88073
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SEQ ID49

SEQ ID70

0	allele 88050 ORMATION allele	FEATURE: NAME/KEY: allele LOCATION: 7277172 OCHER INFORMATION:	N)	DRMATION: allele 160031	ORMATION: allele 150329	FEATURE: NAME/KEY: allele LOCATION: 146345	EATURE:  AME/KEY: allele OCATION: 146328				TINFORMATION: RE: KEY: allele ION: 108471	THE CAME I TOWN.  RE:  (EY: allele  ION: 108308		RE:  KEY: allele  ION: 108106	RE: KEY: allele ION: 106940	FEATURE: NAME/KEY: allele LOCATION: 103806 OTHER INFORMATION:	THER INFORMATION:
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RESULT 12
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APPLICANT: Bouguele
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TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
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PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
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SOFTWARE: Patent.pm
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LOCATION: 90842
OTHER INFORMATION:
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            OTHER INFORMATION:
                          NAME/KEY: allele
LOCATION: 99117
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FEATURE:
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LOCATION: 93714
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LOCATION: 88073
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NAME/KEY: allele
LOCATION: 72794
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TYPE: DNA
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NAME/KEY: allele
LOCATION: 108127
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NAME/KEY: allele

NAME/TON: 150329
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NAME/KEY: allele
'A"TON: 134362
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                   OTHER INFORMATION:
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LOCATION: 88050..88096
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LOCATION: 72771..72817
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LOCATION: 160031
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LOCATION: 134374
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LOCATION: 146328
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LOCATION: 134134
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LOCATION: 108308
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LOCATION: 103806
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NAME/KEY: allele
LOCATION: 93690..93
OTHER INFORMATION:
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LOCATION: 103783..
OTHER INFORMATION:
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LOCATION: 99094..99
OTHER INFORMATION:
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LOCATION: 99075..99121
OTHER INFORMATION: pol
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NAME/KEY: allele
LOCATION: 97130..97177
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LOCATION: 97099..97145
OTHER INFORMATION: pol
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LOCATION: 93690..9:
OTHER INFORMATION:
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OTHER INFORMATION: complement polymorphic fragment 9-1437-325
NAME/KEY:
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OTHER INFORMATION:
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LOCATION: 103783..103828
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LOCATION: 97130..97177
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LOCATION: 97099..97145
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OTHER INFORMATION:
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LOCATION: 106918..106966
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Best Local Similarity
Matches 57; Conserv
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CURRENT FILING DATE: 2002-04-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/091,315 PRIOR FILING DATE: 1998-06-30
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LOCATION: 90842
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: allele
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LOCATION: 103806
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LOCATION: 99098
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LOCATION: 99117
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LOCATION: 106940
OTHER INFORMATION: :
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LOCATION: 90819..90865
OTHER INFORMATION: com
FEATURE:
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                      NAME/KEY: allele
LOCATION: 90819...
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LOCATION: 72771..72817
OTHER INFORMATION: pol:
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LOCATION: 88050..88096
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LOCATION: 72771..72817
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LOCATION: 146328
OTHER INFORMATION:
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LOCATION: 160031
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OTHER INFORMATION:
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LOCATION: 108149
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LOCATION: 108106
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OCATION: 146345
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OCATION: 134362
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OCATION: 134134
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        fragment 99-1437-325
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OTHER INFORMATION:
                                                    NAME/KEY: allele
LOCATION: 108127..108177
                                                                                          FEATURE
                                                                                                         LOCATION: 108127..108177
OTHER INFORMATION: polym
                                                                                                                                                                                             NAME/KEY: allele
LOCATION: 108084..108130
                                                                                                                                                                                                                                                 NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymo
                                                                                                                                                                                                                                                                                                        LOCATION: 106918..1 OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: 106918..106966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 103783..103828
NAME/KEY: allele
                    FEATURE
                                                                                                                                            NAME/KEY: allele
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LOCATION: 106918..106966
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LOCATION: 103783..103828
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OTHER INFORMATION: polymorphic
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LOCATION: 99075..99121
OTHER INFORMATION: pol-
FEATURE:
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LOCATION: 97130..97177
OTHER INFORMATION: pol:
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ
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LOCATION: 99094..99140
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LOCATION: 99094..99140
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LOCATION: 97099..97145
OTHER INFORMATION: pol
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LOCATION: 93690..
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US-10-027-632-231146

Sequence 231146, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231146
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               Sequence 14, Application US/09984827
GENERAL INFORMATION:
APPLICANT: DENEFLE, PATRICE
APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUYERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
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CURRENT APPLICATION NUMBER: US/09/984,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                 560 getetattactttotaactetgtgactttgggcaaatgacttaa 603
                                                                                                                                                                                                                                                                                                                                                                                      500 ggtggtaatatagtgtaagagcacagactctggagccaaactgcctaggttcaaatctta 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 ctaaccatctttgccaatgttgcttaagctttt 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/198,676
FILING DATE: 2000-04-20
APPLICATION NUMBER: US 60/193,483
FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24
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57; Conserv
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Pred. No. 1.7;
0; Mismatches 36;
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                                                                                                                                                                                        ; TYPE: DNA; ORGANISM: Homo sapiens US-09-984-827-14
                                                                                                                  Matches
                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                   SEQ ID NO 14
LENGTH: 7379
                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-04-01 PRIOR APPLICATION NUMBER: 60/254,108
                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
1436 gaccttgggcaagctgcttagtctctct 1463
                                                         1376 gggagtttggagcatacagagctcaagttgaatcctgactttgctacttattggctatat 1435
                55;
                                                                                                                  Conservative
                                                                                                                               29.3%;
                                                                                                                  0;
                                                                                                                            Score 35.2; DB 5;
Pred. No. 0.94;
                                                                                                                  Mismatches
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Gaps

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Search completed: September Job time: 37062 sec ω, 2002, 01:09:44

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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(cgn2_6/ptodata/2/pna/US096A_COMB.seq: *
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/pna/US06_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

Query

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Sequence 316, App Sequence 302, App	Sequence 1897, App Sequence 917, App	2422,	Sequence 145, App	sequence 393, App	sequence 239, App Sequence 239, App	239, 7	1053,		1053	sequence 15, Appl	c	151,	Sequence 1994, Ap	Sequence 135, App	Sequence 1202, Ap	Sequence 609, App	Sequence 10171, A	Sequence 10171, A	Sequence 10171, A	Sequence 9, Appli	Sequence 10, Appl	Sequence 1, Appli	Sequence 4, Appli	Description

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                                                                                                                                       Sequence 1, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
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                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA; ORGANISM: Homo Sapiens US-09-834-291-4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 4
         CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
                                                                                                    APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
 SOFTWARE:
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12 US-60-233-937-211
12 PCT-US01-01334-8121
0 US-99-764-874-8121
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0 US-10-092-400-8123
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1 US-10-092-400-8123
2 US-60-245-228-209
4 US-60-245-228-209
4 US-60-258-272-83
9 US-60-237-889-5424
1 US-09-637-889-5424
9 US-60-208-596-27
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Pred. No. 1.9e-26;
; Mismatches 0;
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Sequence 211, App
Sequence 8121, Ap
Sequence 8121, Ap
Sequence 8123, Ap
Sequence 8123, Ap
Sequence 8123, Ap
Sequence 209, Appl
Sequence 209, Appl
Sequence 2424, Ap
Sequence 281585,
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
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US-60-245-224-9/c
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-722-10
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US-09-997-722-10
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TITLE OF INVENTION: ISOLATI
TITLE OF INVENTION: USES T
TITLE OF INVENTION: USES T
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Best Local S
Matches 120
                                                                                                                                                                                                                                              Sequence 9, Application US/60245224
GENERAL INFORMATION:
                                                       SOFTWARE:
SEQ ID NO 9
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Best Local Similarity
Matches 120; Conserv
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LENGTH: 3212
                                                                                         CURRENT APPLICATION NUMBER: US/60/245,224
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 177
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APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: Patentin version 3.1
ORGANISM: HUMAN
                   TYPE:
                                   LENGTH: 17974
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                                                                       FastSEQ for Windows Version 4.0
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NUCLEIC ACID MOLECULES ENCODING HUMAN RAS-LIKE PROTEINS,
USES THEREOF
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Pred. No. 1.9e-26;
); Mismatches 0;
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                                                                                                                                                                                                                                                                            Sequence 10171, Application US/09922340 GENERAL INFORMATION: APPLICANT: Hyseq, Inc.
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From cDNA Libraries Of Fetal Liver-Spleen and Infant Brain
FILE REFERENCE: 20411-726CON2
CURRENT APPLICATION NUMBER: US/09/353,690
CURRENT FILING DATE: 1999-07-14
CURRENT FILING DATE: 1999-07-14
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 10171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: US 09/217,517
EARLIER FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: US 09/004,182
EARLIER FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 12181
                                                            TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From cDNA Libraries Of Fetal Liver-Spleen and Infant Brain
FILE REFERENCE: 20411-726CON2
CURRENT APPLICATION NUMBER: US/09/922,340
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/533,690
PRIOR FILING DATE: 1998-01-07-14
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
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                                              NUMBER OF SEQ ID NOS:
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LOCATION: (1)...(443)
OTHER INFORMATION: n = A,T,C or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 443
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Pred. No. 0.0034;
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Pred. No. 0.0071;
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APPLICANT:
APPLICANT:
APPLICANT:

Gearing, David P.

APPLICANT: Holtzman, Douglas A.
APPLICANT: Kingsbury, Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(443)
OTHER INFORMATION: n = A,T,C or G
US-09-922-340-10171
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                                              RESULT 8
US-09-726-803-609
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Sequence 10171, Application US/09922340A

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From cDNA Libraries Of Fetal Liver-Spleen and Infant Brain
TITLE OF INVENTION: From cDNA Libraries Of Fetal Liver-Spleen and Infant Brain
FILE REFERENCE: 20411-726CCN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 12181
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10171
LENGTH: 443
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Sequence 609, Application US/09726803 GENERAL INFORMATION:
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 09/217,517
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
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NAME/KEY: misc_feature
LOCATION: (1)...(443)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                   146 TGGAGGAAAATGAAAGGCAATATCGAGAGCCTGGGCTCTGGCATCAGAATGCCTGAGTTC 87
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                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                         Score 43.2; DB 34; Length 443; Pred. No. 0.0071;
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GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Kingsbury, Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFORE
FILE REFERENCE: 1600.2050-001
CURRENT APPLICATION NUMBER: 05/09/726,803
CURRENT FILING DATE: 2000-11-30
                US-60-205-418-135; Sequence 135; Application US/60205418; GENERAL INFORMATION:
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                                                                        RESULT
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; LOCATION: (1)...(518)
; OTHER IMPORMATION: n = A,T,C or
US-09-726-803-609
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                                                                                                                                                                                                                                                                                                Query Match
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   APPLICANT:
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PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 1769
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CURRENT APPLICATION NUMBER: US/09/726,803
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/168,085
PRIOR FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 518
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                             586 agtcatgtggccttggtcatgttacttaacctttct 621
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                                                                                                                                   84 aactaaccatctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                      389 aaggagcatggactttgcagctagactgcctagtttagaatcctggctctgccatgtatt 448
                                                                                                                                                                                                                                                                          Match 36.0%;
Local Similarity 65.6%;
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Beasley, Ellen
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65.6%;
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Pred. No. 0.0075;
0; Mismatches 33;
                                                                                                                                                                                                                                                                        Score 43.2; DB 2
Pred. No. 0.0081;
                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                         DB 29;
                                                                                                                                                                                                                                                        33; Indels
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                                                                                                                                                                                                                                                                                         Length 684;
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GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Jakubowski, Joseph A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
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; ORGANISM: HUMAN
US-60-205-418-135
                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1994
LENGTH: 396
                                                                                                                                                                        Matches
                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 1600.2077-001
CURRENT APPLICATION NUMBER: US/09/824,559
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 60/193,437
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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CURRENT FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 536
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: CLO
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                           151 aagagcgtgaagttgggaaacagactgtctgaatttaaatcctaactctaccacttatta 210
211 gctgtgtgatcttaggaaagttacttaatccttt 244
                       85 actaaccatctttgccaatgttgcttaagctttt 118
                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 aattootgactotgotatttattaactaaccatotttgocaatgttgottaagctttttt 120
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                                                                                                                                                                        62;
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                                                                                                                                                                    Conservative
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66.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.0%;
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                                                                                                                                                               Score 42.8; DB 31; Length 396; Pred. No. 0.0092; 0; Mismatches 32; Indels 0

 Mismatches

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                                                                                                                                                               0;
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US-60-207-583-151/c

Sequence 151, Application US/60207583

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: NUCLEIC ACID MOLECU
TITLE OF INVENTION: NUCLEIC ACID MOLECU
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000598

Ellen ISOLATED HUMAN TRANSPORTER PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, AND USES THEREOF 0,

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RESULT 14
US-09-972-546-15
; Sequence 15, Application US/09972546
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Beasley, TITLE OF INVENTION:
               APPLICANT: STRITTMATTER, STEPHEN M. APPLICANT: CATE, RICHARD L. APPLICANT: SAH, DINAH W.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 32768
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/60/230,445
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LOCATION: (1)...(32768)
OTHER INFORMATION: n = A,T,C or
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NAME/KEY: misc_feature
LOCATION: (1)...(32768
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                                                                                                                                                                                      1184 GCTCTGTTACTTATAAGCTCTGCAACCTCGGGCAGATTACCTAAGTCAGTTT 1133
                                                                                                                                                                                                                                                              1244 GAGGGACAGAGATGGTAAAAACATGGACTTGGAAGCCAGACCGTCTGGGTTTGAATCCTG 1185
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                                                                                                                                                                                                                                                                               9 gggggtatggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctg 68
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 INVENTION:
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NOGO RECEPTOR HOMOLOGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-09-06
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                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                  Score 41.6; DB Pred. No. 0.082; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        DB 62;
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; LOCATION: (87944). (88043);
; OTHER INFORMATION: a, t, c, (
; NAME/KEY: modified_base
; LOCATION: (111030)..(111129);
; OTHER INFORMATION: a, t, c, (
US-09-972-546-15
RESULT 15
US-60-212-358-85
                                                             Db 110864 gctctgttacttataagctctgcaacctcgggcagattacctaagtcagttt 110915
                                                                                                                              Db 110804 gagggacagagatggtaaaaacatggacttggaagccagaccgtctgggtttgaatcctg
                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: (75528). (75627)
OTHER INFORMATION: a, t, c, 9
NAME/KEY: modified_base
LOCATION: (87944)
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                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                Matches
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PRIOR APPLICATION NUMBER: 60/238,361
PRIOR FILING DATE: 2000-10-06
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CURRENT APPLICATION NUMBER: US/09/972,546
CURRENT FILING DATE: 2001-10-06
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OTHER INFORMATION: a, t, c,
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c,
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OTHER INFORMATION: a, t, c,
NAME/KEY: modified_base
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NAME/KEY: modified_base
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LOCATION: (49000)..(49099)
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OTHER INFORMATION: a, t, c,
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60.7%;
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 Mismatches

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                                                                                                                                                                                                  Indels
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Sequence 85,

Application US/60212358

0;

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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
ITITLE OF INVENTION: HORMONE RECEPTOR
ITITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000684
CURRENT APPLICATION UNMBER: US/60/212,358
CUURRENT FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 324
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 85
SEQ ID NO 85
SEQ ID NO 85
CORGANISM: HUMAN
US-60-212-358-85

QUERY MATCh
Best Local Similarity 64.2%; Pred. No. 0.089;
MATChes 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
MATCHES 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
MATCHES 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
MATCHES 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
MATCHES 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
MATCHES 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
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MATCHES 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
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MATCHES 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
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MATCHES 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score diatribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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 383533 seqs, 122816752 residues
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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  US-08-206-176-5
US-08-766-858A-4
US-07-797-556-1
US-08-308-881-1
US-09-058-263-1
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US-09-058-264-1
US-09-058-264-1
US-09-058-264-1
US-08-795-473B-4
US-08-795-473B-4
US-08-781-891-743-16
US-08-916-935-464-4
US-07-928-464-4
PCT-US93-07347-4
US-07-928-464-5
PCT-US93-07347-3
PCT-US93-07347-3
PCT-US93-07347-3
PCT-US93-07347-6
US-08-003-311B-6
US-08-003-311B-6
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US-08-003-311B-6
US-08-003-311B-6
US-08-003-311B-6
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APPLICATION NUMBER: US/U8/200 FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: PARKET, GATY E REGISTRATION NUMBER: 31-648 REGISTRATION NUMBER: 93-7 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-548-2329 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 10564 base pairs TYPE: nucleic acid STRANDEDNESS: double TYPE: DNA (genomic) INMEDIATE SOURCE: CLONE: human fibrinogen gammn FEATURE: CDS LOCATION: .2603, 4211.4341 LOCATION: .7703, 9342.9571	RESULT 1  US-08-206-176-5/c  Sequence 5, Application US/08206176  Patent No. 5639940  GENERAL INFORMATION:  APPLICANT: Garner, Ian  APPLICANT: Foster, Donald C  TITLE OF INVENTION: Animals  NUMBER OF SEQUENCES: 27  CORRESPONDENCE ADDRESS:  ADDRESSEB: Zymodenetics, Inc. STREET: 4225 ROOSevelt Way, N.E. CITY: Seattle STATE: WA COUNTRY: USA ZIP: 98105  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:	27.88 27.88 27.88 27.88 27.88 27.88 27.88 27.88 27.88 27.88
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US-08-766-858A-4/c
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                      1708 ATACAGTTTGCATGACTTGGCGAGCTAATCCCCCATAAGGTTCTTGAAGGAATCTGATACT 1649
       1648 CATTACGTAAACAGCCAATCAAGTGATGTAGATGATTTTTT 1608
                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 35:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,858A
FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Crook, Wannell M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 13-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hickey, Erin K.
APPLICANT: O'Connell, William A.
TITLE OF INVENTION: METHODS AND MATERIALS FOR DETECTING
TITLE OF INVENTION: LEGIONELLA PNEUMOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4985 TATTAGTTATGTGGTCTTGGGCAAGTTATTTAACCTTGTGT 4945
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                                    80 tattaactaaccatctttgccaatgttgcttaagctttttt 120
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                                                                                           20 atagaaagagcaggaccttgggagcaagaatatctaagtttaaattcctgactctgctatt 79
                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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ilarity 56.4%;
Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                         Score 30.6; DB 2; Length 1980; Pred. No. 0.24;
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                                                                                                                                          Mismatches
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US-07-797-556-1
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TISSUE TYPE:
                                                                                                                               150 ATGGAAAAAGCATGACATTTAGAAGTAGAAGACTTAGCTTCAAATCCCTACTCCTTCACT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
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MOLECULE TYPE: cD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
TITLE OF INVENTION: Inhibitory Factor
NUMBER OF SEQUENCES: 17
210 TACTAATTTTGTGATTTGGAAATATCCGCGCAAGATGTT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
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LOCATION:
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LOCATION:
                                                                     80 tattaactaaccatctttgccaatgttgcttaagctttt 118
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Local Similarity 55.6%;
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Pred. No. 1.2;
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                                                                                                                                                          Query Match
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TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
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APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
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APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
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ORIGINAL SOURCE:
TISSUE TYPE:
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LENGTH: 2369 base pairs
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ATTORNEY/AGENT INFORMATION:
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TELEX: 756822
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CLASSIFICATION:
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ZIP: 98101
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CITY: Seattle
210 TACTAATTTTGTGATTTGGAAATATCCGCGCAAGATGTT 248
                                                                                                                                                                                                                         NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                           80 tattaactaaccatctttgccaatgttgcttaagctttt 118
                                                                               20 atagaaagagcaggaccttgggagcaagaatatctaagttttaattcctgactcttgctatt 79
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nes 55; Conserv
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Apple Macintosh
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244..309
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310..2369
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                                                                                                                            Score 28.6; DB Pred. No. 1.2; 0; Mismatches
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150 ATGGAAAAAGCATGACATTTAGAAGTAGAAGACTTAGCTTCAAATCCCTACTCCTTCACT 209

20 atagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgctatt 79

Matches

Conservative

23.8%;

Score 28.6; DI Pred. No. 1.2; O; Mismatches

DB 2; Length 2369;

44;

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Gaps

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Best Local Similarity

Query Match

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RESULT 5
US-09-058-263-1
; LOCATION:
US-09-058-263-1
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                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese Kathryn A.
REGISTRATION NUMBER: 32,172
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APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
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APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
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TELEFAX: 756822
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OPERATING SYSTEM: Apple 7
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FILING DATE: 12-SEP-1994
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                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                      TYPE:
                          NAME/KEY:
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                                                                                                                                                                                                                                                                              LENGTH: 2369 base prype: nucleic acid
                                                       LOCATION:
                                                                   NAME/KEY:
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; LOCATION:
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                                    Query Match 23.8%;
Best Local Similarity 55.6%;
       Matches
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APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2369 base pairs
                                                                                                                                                                                                                                                                                   FEATURE:
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ORIGINAL SOURCE:
TISSUE TYPE:
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APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
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STREET: 5.
TTTY: Seattle
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REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 26
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7
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TELEX: 756822
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                         Score 28.6; DI
Pred. No. 1.2;
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Mismatches
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44;
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Indels
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Gaps

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US-09-058-264-1
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US-09-058-264-1
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Patent No. 6010886
GENERAL INFORMATION:
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                             FEATURE:
NAME/KEY:
                                                                                               FEATURE:
                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                               FEATURE:
                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathyyn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TELEFAX: 756822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mosley, Bruce APPLICANT: Cosman, David J. TITLE OF INVENTION: Recepto
                                                                                                                                                                                                                                            ANTI-SENSE: NO
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STREET: 51
                                                               LOCATION:
                                                                              NAME/KEY:
                                                                                                                                                             CLONE: B10G/pDC303
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                                                                                                             LOCATION:
                                                                                                                              NAME/KEY:
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TOPOLOGY: lir
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OPERATING SYSTEM: Apple 7
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                 LOCATION:
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Microsoft Word, Version 5.1a
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               sig_peptide
244..309
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MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                         TELEX: 756822
[NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
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LENGTH: 2369 base pair
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                                                                                                                                                            FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: TISSUE TYPE: human plac
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                                                                 FEATURE:
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                  EATURE:
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                                   LOCATION:
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DEDNESS: single
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51 University Street
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244..2369
sig_peptide
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Pred. No. 1.2;
0; Mismatches 44;
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PCT-US95-06530-1
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Patent No. 6217858
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Best Local Similarity
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                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212)-997-10
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 100-00
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pair
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                                                                     162 ATGGAAAAAGCATGACATTTAGAAGTAGAAGACTTAGCTTCAAATCCCTACTCCTTCACT 221
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 222 TACTAATTTTGTGATTTGGAAATATCCGCGCAAGATGTT 260
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SOFTWARE: MS-DOS EDITOR
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                        80 tattaactaaccatctttgccaatgttgcttaagctttt 118
                                                                                        20 atagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgctatt 79
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                                                                                                                                                                                                                                                                                        TYPE:
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nucleic acid
EDNESS: single
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nilarity 55.6%;
Conservative
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11-FEB-1997
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Pred. No. 1.2;
O; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                    963.1007
                                                                                                                                           Score 28.6; DI
Pred. No. 1.3;
0; Mismatches
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                                                                                                                                                                              DB 4; Length 3085;
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RESULT 11
US-08-733-360A-4/c
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                                                                                                                                                                                              Sequence 4, Application US/08733360A Patent No. 6103525
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                       GENERAL INFORMATION:
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Sequence 79, App
No. 60906
                                                                                                                                                                                                                                                                                                76558 ATCCTGGCTCTGCCGCTTACTAAATAAGCAATCTAGGAAATTATG 76514
                                                                                                                                                                                                                                                                                                                                                                    76618 GTGAAAGGCCATATCACAGTGGCATGGACTAGTCTAGGAGTCCCTCAGGTCTGGGTTTGA 76559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6931
INFORMATION FOR SEQ ID NO: 79:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol L. Francis, Ph.D.
STREET: 285 Hamilton Ave, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                              APPLICANT: Stern, Robert
APPLICANT: Frost, Gregory
APPLICANT: Csoka, Anthony
APPLICANT: Wong, Tim M.
TITLE OF INVENTION: Human Plasma Hyaluronidase
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/781,891 FILING DATE: 27-DEC-1996 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                     63 ttcctgactctgctatttattaactaaccatctttgcccaatgttg 107
                                                                                                                                                                                                                                                                                                                                                                                                    3 ggggaagggggtatggcatagaaagagcaggaccttgggagcaagaatatctaagtttaa 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schellenberg, Gerald D.
VENTION: GENE AND GENE PRODUCTS RELATED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mulligan, John T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28.2; DB 3; Length 87350; Pred. No. 5.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              48; Indels
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; SEQ ID NO 16
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: H. sapiens
US-08-987-743-16
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                                                                        Matches
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Stern, Robert
APPLICANT: Csoka, Anthony
APPLICANT: Frost, Gregory I.
APPLICANT: Wong, Tim M.
TITLE OF INVENTION: Purification and Microsequencing of
TITLE OF INVENTION: Hylauronidase Isozymes
FILE REFERENCE: 9076/088CIP2
CURRENT APPLICATION NUMBER: US/08/987,743
CURRENT FILING DATE: 1997-12-09
CURRENT FILING DATE: 1997-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08987743 Patent No. 6123938
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,360A
FILING DATE: 17-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FIRENCE/DOCKET NUMBER: 06510/063001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 08/733,360 EARLIER FILING DATE: 1996-10-17 NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 327-32.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2372 CCTTTTCTTGCTGCCAACCTTGGGCAACGTGCTTACTCT 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2432 TAGGAGTGCAAGGGCTGTACCCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTC 2373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2517 base pairs
16 tggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgc 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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ZIP: 94301
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                                                                    Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                      23.3%;
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55.0%;
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                                                               Score 28; DB 3; Length 2517; Pred. No. 2; 0; Mismatches 45; Indels
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Pred. No. 2;
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RESULT 14
US-07-928-464-4/c
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Best Local S
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APPLICANT: Wong, Tim. M.
APPLICANT: Wong, Tim. M.
PITTE OF INVENTION: Human Plasma Hyaluronidase
FILE REFERENCE: 9076-088CIP
CURRENT APPLICATION NUMBER: US/08/916,935
CURRENT FILING DATE: 1997-08-21
EARLIER APPLICATION NUMBER: 08/733,360
EARLIER FILING DATE: 1996-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT: Frost, Gregory I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                      ATTORNEY/AGENT INFORMATION:
                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: Mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2372 CCTTTTCTTGCTGTGCAACCTTGGGCAACGTGCTTACTCT 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2432 TAGGAGTGCAAGGGCTGTACCCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTC 2373
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                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 tggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgc 75
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                                          CLASSIFICATION:
                                                     APPLICATION NUMBER: US
FILING DATE: 19920810
                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                   CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: No. 5367065ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 tatttattaactaaccatctttgccaatgttgcttaagct 115
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55; Conserv
                                                                                                                                                                                                                                         19103
Miller, Suzanne E
                                                                                                                                                                                                                                                                                 PA
                                                                                                                                                                                                                                                           U.S.A.
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                                                                                  US/07/928,464
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Pred. No.
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RESULT 15
PCT-US93-07347-4/c
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PCT-US93-07347-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                    REFERENCE/DOCKET NUMBER: UP TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,
              MOLECULE TYPE:
                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 5873 base pair
                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ecker, Joseph R. APPLICANT: Kieber, Joseph J. TITLE OF INVENTION: Constit TITLE OF INVENTION: Mutatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4121 ACCTTGACTGTATATT 4106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4181 AAGAGGAATAAAATATCAAAATCAAAAACATTGGACAACAACTTTCTAATTTAGATTCAA 4122
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LENGTH: 5873 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                 TOPOLOGY:
                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 19930
                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                  1: 5873 base pairs
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PΑ
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                             linear
                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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              DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Constitutive Triple Response Gene and
                                                                                                                                                                                        32,279
                                                                                                                                                                                                                                                                              PCT/US93/07347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                           UPN-1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB 1; Length 5873; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Query Match
Best Local Similarity

23.38;

Score 28; DB 5; Length 5873; Pred. No. 2.6;

Conservative

0; Mismatches

Indels

0;

Gaps

Search completed: September 7, 2002, 18:21:16 Job time: 28770 sec

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Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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length: 2000000000
              N_Geneseq_032802:*

1: /SIDS1/gcgdata/hc
2: /SIDS1/gcgdata/hc
3: /SIDS1/gcgdata/hc
4: /SIDS1/gcgdata/hc
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24: /SIDS1/gcgdata/hc
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120
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0: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA199.DAT: *
1: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA199.DAT: *
2: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA199.DAT: *
2: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1991.DAT: *
3: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1992.DAT: *
3: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1993.DAT: *
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6: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1995.DAT: *
6: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1995.DAT: *
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9: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1999.DAT: *
9: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA1999.DAT: *
2: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA2000.DAT: *
3: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA2001B.DAT: *
3: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA2001B.DAT: *
4: /SIDSI/gcgdata/hold-genesed/geneseqn-embl/NA2001B.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT:*
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(without alignments)
180.856 Million cell updates/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

i.		dip		SUMMARIES	
Result No.	Score	Query Match Length DB		ID	Description
1	38.4		22	ABA15790	Human nervous syst
2	38.4	32.0 9614	22	ABA15792	Human nervous syst
ω	36		22	AAK85994	Human immune/haema
4	35.8		22	AAL03250	Human reproductive
ი 5	35.8		22	AAS31516	Human DNA for a no
о 6	35.8		23	AAH88704	Human DNA sequence
7	35.4		21	AAZ86967	Retinoblastoma bin
8	35.2		21	AAC69140	Human ABC1 gene ex
9	35.2	29.3 9519	22	AAL37169	Human musculoskele
					-

## ALIGNMENTS

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ARESULT ABA15790 ID ABA15790 ID ABA15790 ID ABA1 XX AXX Huma Anti KW A
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human nervous system related polynucleotide SEQ ID NO 8121.
                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200159063-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiparasitic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA15790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA15790 standard; DNA; 9613
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    2000US-0179065.
2000US-0184664.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0190076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                               2001WO-US01334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nephrotropic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy; vaccine;
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ds

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2000US-0231244.
2000US-0231413.
2000US-0232081.
2000US-0232081.
2000US-0232081.
2000US-0232398.
2000US-0232399.
2000US-02332401.
2000US-0233401.
2000US-0233063.
2000US-0233063.
2000US-0234223.
2000US-0234297.
2000US-0234298.
2000US-0234298.
2000US-0234284.
2000US-0234284.
2000US-0234288.
2000US-0236368.
2000US-0236368.
2000US-0236370.
2000US-0236370.
2000US-0237037.
2000US-0237038.
2000US-0237037.
2000US-0237037.
2000US-0237037.
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2000US-0209467

2000US-0214886

2000US-0214886

2000US-0216880

2000US-0216880

2000US-0217487

2000US-0217487

2000US-0217487

2000US-0217487

2000US-0217481

2000US-0220963

2000US-0224518

2000US-0225214

2000US-0225214

2000US-0225266

2000US-0225266
                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0229343.
2000US-0229344.
2000US-0229345.
2000US-0229509.
2000US-0229513.
2000US-0230437.
2000US-0231243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0226868.
2000US-0227182.
2000US-0227009.
2000US-0228924.
2000US-0229287.
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2000US-0225447.

2000US-0225757.

2000US-0225758.

2000US-0225759.

2000US-0225759.

2000US-0226279.

2000US-0226681.
   20-OCT-2000
20-OCT-2000
20-OCT-2000
20-OCT-2000
20-OCT-2000
20-OCT-2000
20-OCT-2000
20-OCT-2000
01-NOV-2000
08-NOV-2000
                                                                                                                                                                                                      17-NOV-2000
01-DEC-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
06-DEC-2000
07-DEC-2000
06-DEC-2000
08-DEC-2000
The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are
                                                                           Nucleic acids encoding useful for preventing, cancers and metastases
                                                    Disclosure;
                                                                                                                                                                             (HUMA-)
                                                                                                                              2001-541565/60.
                                                                                                                                                       CA,
                                                                                                                                                                              HUMAN
                                                                                                                                                       Barash
                                                    SEQ
                                                                                                                                                                                                     2000US-0240960.
2000US-0241785.
2000US-0241786.
2000US-0241808.
2000US-0241808.
2000US-02448221.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246528.
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2000US-0246528.
2000US-0246528.
2000US-0246610.
2000US-0246611.
2000US-0249210.
2000US-0249210.
2000US-0249211.
2000US-0249211.
2000US-0249211.
2000US-0249211.
2000US-0249211.
2000US-024921.
2000US-0251868.
2000US-0251868.
2000US-0251868.
2000US-0251888.
2000US-0251888.
2000US-0251899.
2000US-02540990.
                                                                                                                                                                              GENOME
                                                    IJ
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                                                    NO
                                                                                                                                                                                SCI INC
                                                  8121;
                                                                               g 3224 human
, diagnosing
s -
                                                                                                                                                       Ruben
                                                  1701pp +
                                                                                                                                                       SM;
                                                                                       nervous system antigen polypeptides, and/or treating nervous system
                                                 Sequence Listing; English.
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18-APR-2000
17-JUN-2000
28-JUN-2000
30-JUN-2000
31-JUN-2000
11-JUL-2000
11-JUL-2000
11-JUL-2000
11-JUL-2000
11-JUL-2000
11-JUL-2000
11-JUL-2000
11-AUG-2000
11-SEP-2000
11-SEP-2000
11-SEP-2000
01-SEP-2000
01-SEP

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RESULT/
ABA15792
ID ABA1
XX ABA1
XX ABA1
XX ABA1
XX Huma
XX Huma
XX Huma
XX Inmu
XX Inmu
XX Inmu
XX Inmu
XX Inmu
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                                                                                                                                                                                                     31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiairthritic; cancer; antirheumatic; hapatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiuleer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6036 ctagcaaaatatgattgggtatgtttcttaaactgt 6071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5976
                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200159063-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human nervous system related polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-2002 (first entry)
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2000US-0209467
2000US-0214886
2000US-0215135
2000US-0216647
2000US-021680
2000US-0217487
2000US-0217496
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2000US-0189874.
2000US-0190076.
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2000US-0180628.
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2000US-0205515.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.01); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nephrotropic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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    30-AUG-2000
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01-SEP-2000
05-SEP-2000
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06-SEP-2000
08-SEP-2000
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22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
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26-JUL-2000;
26-JUL-2000;
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14-AUG-2000;
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29-SEP-2000

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02-CCT-2000

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14-AUG-2000;
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2000US-0220963
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2000US-022511
2000US-0225211
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2000US-0226868.
2000US-0227182.
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2000US-0237039.
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2000US-0239935.
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2000US-0234998.
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2000US-0231968.
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2000US-0232080.
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08-NOV-2000;
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11-NOV-2000
01-DEC-2000
01-DEC-2000
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05-DEC-2000
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06-DEC-2000
08-DEC-2000
                        The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune harmonytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, allergies, autoimmune themselves and the second of the cancer of the second of the cancer of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                    Disclosure; SEQ ID NO 8123; 1701pp + Sequence Listing; English
   colitis;
                                                                                                                                                                                                                          Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                                                                                                                                                                                                                       cancers and
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multiple sclerosis, rheumato (c) cardiovascular disorders
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2000US-0251990.
2000US-0254097.
2000US-0259678.
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2000US-0256719.
2000US-0251479.
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2000US-0246613.
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2000US-0246609.
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rheumatoid arthritis and ulcerative disorders such as myocardial ischaem
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RESULT
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                                                                                                                   11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
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07-JUN-2000;
28-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (d) wound healing: (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
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                                                                                          2000US-0186350
2000US-019874
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2000US-0199123
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2000US-0216880
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2000US-0225757.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy; vaccine; metastasis;
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2000US-0229287
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CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) cartivity, and can be used in gene therapy and vaccine production. (I) coroteins and polynucleotides may be used in the prevention, diagnosis and camber the associated with inappropriate (I) expression. For cerample, they may be used to treat disorders associated with decreased cexpression by rectifying mutations or deletions in a patient's genome cuthat affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) corotein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting cuthe nucleic acids into a host cell and culturing the cell to express the collapsose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic cancers from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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17-NOV-2000
17-NOV-2000
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17-NOV-2000;
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08-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                         Nucleic acids encoding useful for preventing, metastasis -
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                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 40806; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                              Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                      ( HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000;
17-NOV-2000;
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2000US-0249297

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                                                                                                                                                                                                                                                                                                                        human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                              Ruben
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Query Match Best Local Matches 63; Similarity Conservative 58 58 . 3%; Score 36; DB Pred. No. 0.17 0; Mismatches 0; 0.17; 45; Length 59060; Indels 0; Gaps 0

Sequence

59060

вP;

14758 A;

13705 C;

13620 G; 16977

T; 0 other;

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RESULT AALO ID AALO ID AALO ID AALO ID AALO XX AALO XX AALO XX Huma XX
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19-MAY-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
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2000US-0225759
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2000US-0226681
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2000US-0227109
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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          human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections;
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                                                                                                                                                                                                                                                                                                                               4940 aaaagcacggactctggaaccagtctgtctgaatttgaatcctagctctgccaattacta 4999
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13046 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a \mid medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen
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                                                                        Human; secreted extracellular matrix protein; ds; immunomodulatory; Anti-HU; antianemic; antischeumatic; antischerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immune/autoimmune disease; HIV infection; anaemia;
                                                                                                                                        Human DNA
                                                                                                                                                                 04-DEC-2001
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58; Conservative
                                                                                                                                      for a novel extracellular matrix protein,
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2000US-025198
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2000US-02519978
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2000US-0249300
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2000US-0249264
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2000US-0250391
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2000US-0249297
 immunogen;
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 gene
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                                                                                                                                                                                                                                                                                                                                                                                 0;
therapy;
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  antisense;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
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   22-AUG-2000

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23-AUG-2000

01-SEP-2000

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26-JUL-2000;
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07-JUL-2000;
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04-FEB-2000;
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14-AUG-2000;
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14-AUG-2000;
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2000US-0216847.

2000US-0216880.

2000US-0217487.

2000US-0217496.

2000US-0218290.

2000US-0220963.

2000US-0220964.

2000US-0224518.

2000US-0224518.
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2000US-0198123.
2000US-0205515.
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2000US-0232399.
2000US-0232400.
2000US-0232401.
              2000US-0234223.
2000US-0234274.
2000US-0234997.
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2000US-0230437
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2000US-0228924
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2000US-0226279
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2000US-0214886
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2000US-0189874
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29-SEP-2000; 29-SEP-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000;

2000US-0236802. 2000US-0237037. 2000US-0237038. 2000US-0237039.

2000US-0236369 2000US-0236370

02-OCT-2000; 02-OCT-2000;

2000US-0239935 2000US-0239937

2000US-0237040

2000US-0240960

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RESULT 6
AAH88704/c
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Best Local S
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                      13-JAN-2000; 2000US-0175854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8107 AAAAGCACGGACTCTGGAACCAGTCTGTCTGAATTTGAATCCTAGCTCTGCCAATTACTA 8048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation, support of cell culture of primary tissues, modulation of for example
                                                                                         11-JAN-2001; 2001WO-IB00116
                                                                                                                                                                                                                                                                                                                                                                                                                       Single nucleotide polymorphism; SNP; biallelic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8047 ACTGTGTGACCTTGGGCAAGTTACTTAGCTTCTCT 8013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SPs. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/activities and the control of the SPs and as diagnostic agents for detecting the presence of SPs in samples.
                                                                                                                                                                        19-JUL-2001
                                                                                                                                                                                                                                           WO200151659-A2
                                                                                                                                                                                                                                                                                                                                                                                      central nervous system disorder; CNS; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human DNA sequence SEQ ID 544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH88704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH88704 standard; DNA; 160755 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 595; 577pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 actaaccatctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vention relates to isolated nucleic acid molecules encoding human secreted extracellular matrix proteins (SPs). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 61.: 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.8%;
61.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35.8; DB 22; Pred. No. 0.12;
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); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    human;
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13-OCT 2000
13-OCT 2000
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217-NOV 2000

2000US-0246526. 2000US-0246527. 2000US-0246528.

2000US-0241721.
2000US-0241785.
2000US-0241786.
2000US-02418787.
2000US-0241808.
2000US-0241809.
2000US-024181209.
2000US-024617.
2000US-0246474.
2000US-0246475.
2000US-0246477.

17-NOV-2000; 11-NOV-2000; 01-DEC-2000; 01-DEC-2000; 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000;

2000US-0250160.
2000US-0250391.
2000US-0251981.
2000US-0251988.
2000US-0251479.
2000US-0251856.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251990.
2000US-0251990.
2000US-0251997.

17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

2000US-0249211.

2000US-0249208

2000US-0246611 2000US-0246610 2000US-0246532

17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

2000US-0249218. 2000US-0249244. 2000US-0249264. 2000US-0249264. 2000US-0249265. 2000US-0249297. 2000US-0249299. 2000US-0249290.

GENSET

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RESULT
AAZ86967
ID AAZ8
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to biallelic markers derived from human genes involved in central nervous system (CNS) disorders (see AAH88161-AAH88702). The markers have a single nucleotide polymorphism (SNP) and are useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set genetic markers in a biological sample, where the markers comprise at least one CNS disorder related marker. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotides, useful for genotyping nucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker \ \ _{|}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483085/52.
                                                                                                                                                                                                                                                                                                                               RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;
diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA286967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 160755 BP; 43057 A; 36601 C; 38189 G; 42727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST )
          Novel nucleic acid and polymorphic markers used for diseases, especially those involving abnormal cell differentiation -
                                                                                                                                                      30-JUN-1998;
10-DEC-1998;
                                                                                                                                                                                                                              06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                         Retinoblastoma binding protein-7 genomic DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ86967 standard; DNA; 162450
                                                                                               Bougueleret L;
                                                                                                                           (GEST ) GENSET
                                                                                                                                                                                                  30-JUN-1999;
                                                                                                                                                                                                                                                           WO200000607-A1
                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                   lymphoma; ds.
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                                                                    2000-117170/10
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                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                        98US-0091315
98US-0111909
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57.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
                                      for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |Length 160755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                        r diagnosis of proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T; 181 other;
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                            and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the retinoblastoma binding protein-7 (RBP-7) genomic sequence of the invention. The RBP-7 coding sequence and regulatory sequences are useful for the recombinant production of the protein and for expressing heterologous nucleic acids. Primers and probes derived from the RBP-7 nucleotide sequence (e.g. AAZ87035-Z87099) are useful for DNA amplification and detection methods. RBP-7 biallelic markers (see AAZ8693-Z87034) are useful for diagnosis of disease related to alteration in the regulation or in the coding regions of the RBP-7 gene and for prognosis/diagnosis of an eventual treatment with therapeutic agents, especially agents acting on pathologies involving abnormal cell proliferation and/or differentiation, these include the process of the contract of the cont
                                                                                                                                                                                                                                15-MAR-1999;
08-JUN-1999;
17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers, including breast cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, lung cancer, prostate cancer, various leukaemias, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ABC1 cholesterol transporter; chromosome 9931; ATP-binding cassette; HDL deficiency disorder; high density lipoprotein; Tangier disease; TD; familial HDL deficiency; FHA; polymorphism; cardiovascular disease; coronary artery disease; coronary restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prognosis; prophylaxis; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cerebrovascular disease; peripheral vascular disease; Alzheimer's disease; Niemann-Pick disease; Huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ABC1 gene exons 23-28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphomas. RBP-7 antibodies are useful as diagnostic agents.
                           WPI; 2000-587528/55
                                                                        Hayden MR,
                                                                                                                         (UYBR-) UNIV BRITISH COLUMBIA. (XENO-) XENON BIORESEARCH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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                                                                                                                                                                                                                                                                                                                                    15-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
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                                                                           Wilson AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                    2000WO-IB00532
                                                                                                                                                                                                        99US-0124702.
99US-0138048.
99US-0139600.
99US-0151977.
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                                                                              Pimstone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis;
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RESULT
AAL37169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC transgenic cells and non-human animals comprising human ABC1 nucleic cardidy, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression cc cardiovascular disease comprising the administration of an expression cc encountry and a cative fragment thereof. The invention also cc encountries compounds which mimic ABC1 activity, compounds which cc trimulate ABC1 expression and methods of screening for such compounds. In further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the CC prevent cardiovascular disease due to polymorphisms in the CC cerebrovascular disease, especially coronary artery disease, cerebrovascular disease, especially coronary artery disease, cerebrovascular disease, especially coronary artery disease, disease. They may also be used in the treatment of diseases, Niemann-Pick CC disease. They may also be used in the treatment of disease, Niemann-Pick CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAM10005.1 and X75926, and the nucleic The present sequence represents a fragment of the human ABC1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the human ABC1 cholesterol transporter protein C (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is C a member of the ATP-binding cassette (ABC transporter) superfamily of C proteins, and plays a crucial role in cholesterol transport, particularly convolved in cholesterol trafficking in monocytes and fibroblasts, being C intracellular cholesterol trafficking in monocytes and fibroblasts, being C involved in cholesterol efflux from the cell. The gene encoding ABC1 is coated on chromosome 9931, and mutations in this gene are associated C with two genetic HDL (high density lipoprotein) deficiency disorders, C Tangler disease (TD) and familial HDL deficiency (FHA). These diseases C are distinguishable in that TD is an autosomal recessive disorder, while C that is inherited as an autosomal dominant trait. Low levels of HDL ("good C cholesterol") in the blood correlate with a high risk of cardiovascular C disease, particularly coronary artery disease, but also cerebrovascular C clasese, particularly restenosis, and peripheral vascular disease.

C cardiovascular disease. The invention provides genetic constructs and c transgenic cells and non-human animals comparising human animan animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                  Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antipungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder
                                                                                                                   Human musculoskeletal system related polynucleotide SEQ ID NO 3534.
                                                                                                                                                            08-JAN-2002 (first entry)
                                                                                                                                                                                                                                            AAL37169 standard;
                                                                                                                                                                                                                                                                                                                                           5906 gaccttgggcaagctgcttagtctctct 5933
                                                                                                                                                                                                                                                                                                                                                                                                                   5846 gggagtttggagcatacagagctcaagttgaatcctgactttgctacttattggctatat 5905
        neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7052 BP; 1816 A; 1465 C; 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising exonic sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 12; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
                                                                                                                                                                                                                                                                                                                                                                 92 atctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                              DNA;
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      infection; human;
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disorder; cardiovascular disorder; secreted protein;
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08-SEP-2000;
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08-SEP-2000;
12-SEP-2000;
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07-JUN-2000;
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17-MAR-2000;
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2000US-0232401.
2000US-0233063.
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2000US-0225266.
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2000US-0225270.
2000US-02252447.
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2000US-0231242.
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2000US-0229509
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2000US-0227182
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2000US-0209467
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26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
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2000US-0235844.
2000US-0235836.
2000US-0235836.
2000US-0236367.
2000US-0236369.
2000US-0236370.
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2000US-0236370.
                            2000US-0249265

2000US-0249297

2000US-0249300

2000US-0249300

2000US-0250391

2000US-0250391

2000US-0251030

2000US-0251479

2000US-0251479

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CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC protein or gene therapy. The genes are isolated from a range of human CC tissues disclosed in the specification. The nucleic acids, proteins, CC antibodies and (antiagonists are useful in the diagnosis, treatment CC antibodies and (antiagonists are useful in the diagnosis, treatment CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and CC other cancers of the adrenal gland, bone, bone marrow, breast, CC gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; CC constantial ischaemias; (d) wound CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; CC constantial fractions diseases such as viral, bacterial, fungal and
Matches
                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis -
                                                                                                                   Sequence 9519 BP; 2702 A; 1682 C; 1664 G; 3471 T; 0 other;
                                                                                                                                                                                        parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                    Y Match 29.3%;
Local Similarity 62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO 3534;
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Score 35.2; DB Pred. No. 0.18; 0; Mismatches
                                           DB 22; Length 9519;
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Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                   Tumour suppressor gene derived chemically modified sequence #78
                                                                                                                                                                                                                   AAS46356 standard; DNA; 14537 BP
                                                                                                                                                                       AAS46356;
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                                                                                                                     18-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                            71 tctgctatttattaactaaccatctttg 98
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RESULT 10 AAS46356/c

ΩV B QΥ

3888

cytosine methylation; ds.

15-MAR-2000; 2000DE-1013847

20-SEP-2001

WO200168912-A2

15-MAR-2001;

2001WO-EP02955

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RESULT
AAK65581
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Best Local Similarity
"~+~hes 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a nucleic acid comprising a sequence of 18 cc bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an CC cancers and tumours. The probes can also be used in a methylation state CC and/or therapy of existing diseases associated with CpG dinucleotides e.g. CC cancers and tumours. The probes can also be used in a method for CC and/or therapy of existing diseases or the predisposition to specific CC and/or therapy of existing diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be CC differences serving as basis for diagnosis and/or prognosis events which cCC are disadvantageous to patients. The present sequence is one of the CC complementary sequences derived from tumour suppressor genes and CCC complementary sequence with even numbered Seq ID numbers are the CCC complementary sequence of the orresponding odd numbered sequence (e.g. ID 2 and ID) ID 345 and ID 455. excent for those whose arterior sequence (e.g. ID 2 and ID) ID 345 and ID 455. excent for these whose arterior sequence (e.g. ID) and ID 100 control of the corresponding odd numbered sequence (e.g. ID) and ID 100 corresponding odd numbered sequence (e.g. ID) and ID 100 corresponding odd numbered sequence (e.g. ID) and ID 100 corresponding odd numbered sequence (e.g. ID) and ID 100 corresponding odd numbered sequence (e.g. ID) and ID 100 corresponding odd numbered sequence (e.g. ID) and ID 100 corresponding odd numbered sequence (e.g. ID) and ID 100 corresponding odd numbered sequence (e.g. ID) are corresponding odd numbered sequence (e.g. ID) are corr
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
              Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
      cytostatic; gene therapy; vaccine;
                                             Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20393
                                                                               06-NOV-2001
                                                                                                             AAK65581;
                                                                                                                                         AAK65581 standard;
                                                                                                                                                                                                                 1276 TATTAACAATATAACCTTAAATAAATTACTTAATCT 1241
                                                                                                                                                                                                                                                                                1336
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14537 BP; 3628 A; 495 C; 3778 G; 6636 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is missing).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 78; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-602752/68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                  80 tattaactaaccatctttgccaatgttgcttaagct 115
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                                                                                                                                                                                                                                                                                          atagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctgctatt 79
                                                                                                                                                                                                                                                                           and ID1, ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                            (first entry)
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                         DNA; 56632 BP
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Pred. No. 0.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                      0;
    metastasis;
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14-SEP-2000;
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07-JUL-2000;
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14-JUL-2000;
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2000US-0229513.

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2000US-0227182.
2000US-0227009.
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2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-019076.
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2000US-0229287
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2000US-0225266
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2000US-0218290.
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13-OCT-2000;
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27-SEP-2000;
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01-NOV-2000;
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                                        2000US-0251479.
2000US-0251856.
2000US-0251868.
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2000US-0249265.
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2000US-0235834.
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2000US-0241221.
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2000US-0237037.
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2000US-0256719.
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2000US-0249300.
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2000US-0249218.
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51064 tctgccacttagtagccatgtgaatttg 51091

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                                                                                 QΥ
                                                                                                                                                                                                                                                                 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) corrections and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For comple, they may be used to treat disorders associated with decreased comple, they may be used to treat disorders associated with decreased comple, they may be used to treat disorders associated with decreased comple, they may be used to treat disorders associated with decreased complement the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) complement the patients own production of (I). Additionally, (I) complement the patients own produce the secreted (I), by inserting complement cacids into a host cell and culturing the cell to express the contain. (I) proteins and polynucleotides may be used to prevent, complement in the case of haematopoietic-derived cells. AAK64703 concers and cancer metastases of haematopoietic antigen genomic concers from the present invention. AAK54942 to AAK54950 and AAM62169 corporates and cancers used in the exemplification of the present invention.
                                                                                                                             Matches
                                                                                                                                               Query Match
Best Local
                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483426/52.
                                                                                                                                                                                                                              Sequence 56632 BP; 17016 A; 8910 C; 10552 G; 20154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                               11 gggtatggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgac 70
  71 tctgctatttattaactaaccatctttg 98
                                                                                                                             55;
                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 20393; 3071pp + Sequence Listing; English.
                                                                                                                             Conservative
                                                                                                                                                 29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM;
                                                                                                                               0,
                                                                                                                                                 Score 35.2;
Pred. No. 0.
                                                                                                                               Mismatches
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                                                                                                                                                                         DB
                                                                                                                                 33;
                                                                                                                                                                       Length 56632;
                                                                                                                                 0;
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RESULT
AAF92831
01-SEP-1999;
15-MAR-2000;
23-JUN-2000;
                                                                                                                             High density lipoprotein-cholesterol; HDL-C;
                                                                                                                                               Human ABC1 genomic DNA.
                                                                                                                                                                               AAF92831;
                                                                                                                                                                                               AAF92831 standard; DNA; 183999 BP
                                                              01-SEP-2000; 2000WO-IB01492.
                                                                               08-MAR-2001
                                                                                              WO200115676-A2
                                                                                                               Homo sapiens.
                                                                                                                                                               17-MAY-2001
      (UYBR-) UNIV BRITISH COLUMBIA. (XENO-) XENON GENETICS INC.
                                                                                                                                                                                                               12
                             ; 99US-0151977.
; 2000US-0526193.
; 2000US-0213958.
                                                                                                                                                              (first entry)
                                                                                                                                cardiovascular; ABC1;
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  New peptide useful as a marker for the diagnosis
                                                                                                                                                   24-MAR-2000;
29-MAR-2000;
                                 WPI; 2001-451856/48.
                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                        15-MAY-2000;
                                                                                                                                                                              14-MAR-2000;
                                                                                                                                                                                            14-JAN-2000;
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                                                                                                                                                                                                                                                19-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABCl expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition self lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                                                                                                                                                                                                                                                                                       Human; breast cancer; cell marker; cytostatic; ss
                                                                                                                                                                                                                                                                                                                                                                              07-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL13265 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates or RXR-mediated transcriptional activity -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                                                                                                                                                                 breast cancer expressed polynucleotide 5722.
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                                                          Xu Υ,
                                                                                                           2000US-0189167
2000US-0192099
2000US-0193480
2000US-0205230
2000US-0201315
2000US-0220534
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                                                          Wang
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of breast cancer
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          The invention relates to human breast cancer expressed polynucleotides (AALD/544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for
                                                                                                                                                                                                                                                                                                    14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
                                                                                                                               New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                   WPI; 2001-451856/48.
                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                      15-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                          10-JAN-2001; 2001WO-US00798
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200151628-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; breast cancer; cell marker; cytostatic; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL22135 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    breast cancer expressed polynucleotide 14592.
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diagnosing, monitoring, characterising treating
                                                                                                                                                                                             Xu Y, Wang Y,
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2000US-0192099
2000US-0193480
2000US-0205230
2000US-0205230
2000US-0221315
2000US-0220534
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                                                                                                     2627; 3695pp; English.
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Pred. No. 0
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RESULT 1
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     Query Match
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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
11-MAR-2000;
11-MAR-2000;
11-MAY-2000;
11-MAY-2000;
07-JUN-2000;
28-JUN-2000;
28-JUN-2000;
21-JUL-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human musculoskeletal system related polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JAN-2002 (first entry)
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acttacttactaatattct 109
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 2000US-0179065
2000US-0184664
2000US-0184664
2000US-0184664
2000US-0198174
2000US-0199123
2000US-0199123
2000US-0199123
2000US-0214886
2000US-0214886
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2000US-0214687
2000US-02146880
2000US-02146880
2000US-0217496
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2000US-0225266
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2000US-0225266
2000US-0225268
2000US-0225277
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Pred. No. 0.13;
0; Mismatches 28;
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     14-AUG-2000

18-AUG-2000

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22-AUG-2000

22-AUG-2000

23-AUG-2000

23-AUG-2000

01-SEP-2000

01-SEP-2000
 14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
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25-SEP-2000;
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20-OCT-2000;
02-OCT-2000;
03-OCT-2000;
03-OCT-2000;
03-OCT-2000;
04-NOV-2000;
06-NOV-2000;
08-NOV-2000;
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14-SEP-2000;
14-SEP-2000;
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2000US-0227009

2000US-0228924

2000US-0229287

2000US-0229343

2000US-0229344

2000US-0229345

2000US-0229313

2000US-0229313

2000US-0229313

2000US-0230438

2000US-0230438
 2000US-023397
2000US-0232398
2000US-0232401
2000US-0233063
2000US-0234274
2000US-0234274
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2000US-0234283
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2000US-0234998
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2000US-0232080.
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2000US-0231968.
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2000US-0231244.
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2000US-0225759.
2000US-0226279.
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2000US-0226868.
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17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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2000US-0251479.
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2000US-0249297.
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Rosen CA, Barash SC, Ruben SM;

WPI; 2001-451937/48.

Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.

Example 2; SEQ ID NO 2665; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins CC (ABB3087-ABB04109) associated with the musculoskeletal system useful CC for preventing, treating or ameliorating medical conditions e.g. by CC protein or gene therapy. The genes are isolated from a range of human CC tissues disclosed in the specification. The nucleic acids, proteins, CC antibodies and (ant)agonists are useful in the diagnosis, treatment CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and CC other cancers of the adrenal gland, bone, bone marrow, breast, CC gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; CC colling; (e) neurological diseases e.g. cerebral anoxia and epilepsy; CC anaemia; (i) merological diseases such as viral, bacterial, fungal and CC naraeitic infections diseases such as viral, bacterial, fungal and

parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direfrom WIPO at ftp.wipo.int/pub/published\_pct\_sequences. format directly

Sequence 4171 BP; 1079 A; 1015 C; 1025 G; 1052 T; 0 other;

28.5%; Score 34.2; DΒ 22; Length 4171;

Query Match

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В
                                           Best Local Similarity 60.0 Matches 57; Conservative
   997
          aaggacagggactctggaatccagcagttgtgagtttgaattctgcctcatctcctgact 1056
                                                     60.0%;
                                           Pred. No. 0.29; 0; Mismatches
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Search completed: September Job time: 29921 sec 2002, 18:40:27

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Вþ

1057 agctttgtgaccttggccaagtcgcttaagcctgt 1091

84 aactaaccatctttgccaatgttgcttaagctttt 118

Human DNA s Human DNA Human DNA Homo sapi Homo sapi

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Maximum Match 100
Listing first 45
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1: gb_ba:*
2: gb_htg:
3: gb_in:*
                Match Length
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Gapop 10.0 , Gapext 1.0
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H.sapiens CD95 gene :
X87625
X87625.1 GI:902311
2 (bases 1 to 2344)
Rudert,F.H.
Direct Submission
Submitted (26-MAY-1995) F.H. Rudert, Genesis Research &
Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2344)
Rudert,F., Visser,E., Forbes,L., Lindridge,E., Wang,Y. and
                                                                                            Identification of a silencer, enhancer, in the human CD95 (Fas/APO-1) gene DNA Cell Biol. 14 (11), 931-937 (1995)
                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                    beta interferon; CD95 gene; silencer.
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AC016478
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AC0168631 Homo sapi
AL110502 Human DNA
AL138932 Homo sapi
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AC015685 Homo sapi
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AC015687 Homo sapi
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AC013607 Homo sapi
AL0162423 Human DNA
AL1362427 Homo sapi
AC013647 Homo sapi
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AC073148 Homo sapi
AL355852 Human DNA
AC018803 Homo sapi
AC090587 Homo sapi
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Sequence 4 from Patent DE19847779.
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/note="lysozyme silencer 1"
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/map="q24.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enguiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 31, 2001 this sequence version replaced gi:14161146.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw:, Sw:15 SW:15 SPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blakey,S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL157394 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DNA sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1 from Patent DE19847779. AX026089
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/db_xref="taxon:9606"
784 c 809 g 84
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Pred. No. 4.3e-25;
Pred. No. 4.3e-25;
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KEYWORDS
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AUTHORS
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RP11-399019 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
 Uenishi, H.
Complete s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is the entire insert of clone RP11-399019 The true left end of clone RP11-496H23 is at 166408 in this sequence. The true right end of clone RP11-304I5 is at 18704 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mapping Group.
                                                                   Yang, Y.G., Ohta, S., Yamada, S., Shimizu, M
Diversity of T cell receptor delta-chain
one-month-old pig
J. Immunol. 155 (4), 1981-1993 (1995)
                                                                                                                                                                                                      I (sites)
Thome,A., Saalmuller,A. and Pfaff,E.
Molecular cloning of porcine T cell receptor alpha, beta,
Molecular cloning of porcine T cell receptor alpha, beta,
                                                                                                                                                                                                                                                                                                                                                                                                                                          AB053451
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                 Sus scrofa DNA.
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/note-"Sequence from AC015461 sequenced by WIBR."
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100119. .100156
sequence of
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/db_xref="taxon:9606"
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105973. .105989
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segments of joining
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Pred. No. 3.3e-25;
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Direct Submission
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porcine TCR gene alpha/delta locus
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8371. .8427
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<11129. .>11187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAB83178.1"
/db_xref="GI:18147395"
/translation="TLMAHFIFGNGTQLRVEP"
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/db_xref="GI:18147393"
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/chromosome="7"
/note="putative recombination recognition sequence"
join(14002. .14280,14849. .14914,15573. .15685)
/standard_name="TCR delta chain constant region"
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/db_xref="GI:18147396"
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/note="putative"
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/db_xref="GI:18147394"
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                                                                                                                        /translation="SWDTRQMYFGAGTKLFVEP"
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20647. .:
                                                       complement(join(20205. .20512,20767. .20800))
/standard_name="TCR delta-5 chain variable region"
complement(20513. .20766)
/standard_name="TCR delta-5 chain variable region"
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complement(join(<20205. .20512,20767. .20800))</pre>
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complement(20205. 20512)
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20198. .20204
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/note="3' untranslated
putative"
/citation=[1]
                                           /note="putative"
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19545. .19550
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19628. .19633
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/note="putative"
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/note="TCR delta chain constant region
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/note="putative"
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/db_xref="GI:18147397"
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/citation=[1]
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join(<14002. .14280,14849. .14914,15573. .15685)
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AC073148/c
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TITLE
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                                                                               Direct Submission
Submitted (29-NOV-2000) Genome
University School of Medicine,
Direct Submission Submitted (09-MAY-2001) Department of Genetics, Washington
                                     Waterston, R
                                                                    мо 63108,
                                                                                                                               Waterston, R.H.
                                                                                                                                                                                                                             Waterston, R.H.
                                                                                                                                                                                                                                                                      The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                        Waterston, R.H
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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complement(20767.
/note="putative
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Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Homo sapiens chromosome 7 clone RP11-801B4, complete sequence.
AC073148
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/note="putative"
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<28817. .>28873
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<27821. .>27880
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/note="putative"
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Sequencing Center, Washington 4444 Forest Park Parkway, St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 12, 2001 this sequence version replaced gi:12964290.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTACCTAACTTTGGGCAAGTTTCTTTAACCTCT 10735
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On Nov 29, 2000 this sequence version replaced gi:11128450.
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL355852 128765 bp DNA | linear PRI Human DNA sequence from clone RP11-403E24 on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:http://genome.wustl.edu/gsc/index.shtml Contact: submissions@watson_wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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/db_xref="taxon:9606"
/chromosome="7"
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Pred. No. 0.0006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RP11-403E24 It may be shorter because we sequence overlapping RP11-403E24 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-403E24 is at 1 in this sequence. The true left end of clone RP11-284B18 is at 128666 in this sequence. The true right end of clone RP11-33N11 is at 69175 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \tt RP11-403E24 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MER91C repeat: matches 15. .139 of consensus"
6875. .7385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="16 copies 2 mer ct 100% conserved" 11715. .11918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 45. .147 of consensus" complement(12973. .13643)
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                                                                                                                                         /note="L2 repeat: matches 2589. .2748 of consensus"
17552. .17815
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                                            /note="L2 repeat: matches 2252.
18562. .18822
                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 8. .216 of consensus"
                                                                                                                                                                                                                                                                                                                                                     /note="17 copies 2 mer ct 94% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                    /note="L2
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                        /note="L2 repeat: matches 1630. .1882 of consensus"
                                                                                                                        /note="match:
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                           /note="L2 repeat: matches 2364. .2750 of consensus"
55251. .55292
                                                                                          /note="1.2 repeat: matches 2668. .2750 of consensus" 52330. .52415
/note="5S repeat: matches 1. .42 of consensus"
                                                                                   /note="L2_repeat: matches 1999. .2707 of consensus"
                                                                                                                                                                                                                                                /note="L1PA3 repeat: matches 2. .776 of consensus" 52097. .52180
                                                                                                                                                                                                                                                                                                                                     /note="L2 repeat: matches 2572. .2634 of consensus"
46069. .51314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L1 repeat: matches 3467. .3570 of consensus"
42648. .44277
/note="L1MB4 repeat: matches 4023. .5667 of consensus"
43387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1M4 repeat: matches 2508. .2689 of consensus"
42537. .42636
/note="L1 repeat: matches 3467. .3570 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1MEc repeat: matches 2012. .2254 of consensus 42212. .42343
                                                                                                                                                                                                                                                                                                          /note="L1PA3 repeat: matches 900. .6146 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="LIP repeat: matches 3663, .3772 of consensus"
35265, .35365
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/note="L2 repeat: matches 2042. .2135 of consensus" 20593. .21070
                                                                                                                                                                                                                                                                                                                                                                                               'note="MER47A repeat: matches 1. .366 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="L1MB4 repeat: matches 5654. .6163 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluJb repeat:
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35143. .35252
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|2345. .42525
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#1313. .41618
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29629. .30212
/note="LLP repeat: matches 2. .595 of consensus"
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/note="L1MB4 repeat: matches 6095. .6180 of consensus"
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i5361. .37144
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/note="LLME1 repeat: matches 5558. .6033 of consensus"
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67;
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Submitted (20-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                      Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                        Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                             MO 63108, USA
On Mar 13, 2000 this sequence version replaced gi:6606060
                                                                                                                                                                                                                                                                                                           Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162043 bp DNA linear HTG 07-. HOMO sapiens chromosome 11 clone RP11-348A20, WORKING DRAFT SEQUENCE, 23 unordered pieces. AC018803
                                                                                                                                                                                                                                                                                                                                            Unpublished
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/note="THEIC-internal repeat: matches 4. .309 of consensus"
65007. .65373
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/note="THE1-INTERNAL repeat: matches 694. .791 of
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61467..61997
/note="LLPA13 repeat: matches 5629..6155 of consensus"
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Consensus quality: 153397 bases at least
Consensus quality: 158868 bases at least
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Insert size: 159843; sum-of-contigs
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           /note="assembly_name:Contig11" 3240. .4924
                                     /note="assembly_name:Contig10"
1504. .3139
                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                 1. .162043
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                                                                            /clone="RP11-348A20"
/note="assembly_name:Contig12"
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117239: contig of 13322 bp in le
117339: gap of unknown length
117339: contig of 21991 bp in le
139330: contig of 21991 bp in le
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                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                            RESULT
AC090587
                                                                                                                                                                                                                                        QΥ
                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                              Db 145826 CTATTTCCTAGCTGTGTAACCCTGAAAAATTGCTTAACCTCTGT 145782
                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                   Db 145886 ATGTGGTAGAAAGCACATAAACTCTGGCGCCAGACAAACTAAGGTCAAATCCTGATTTTG
            REFERENCE
                                                                                                       ACCESSION
                                                                                                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
  AUTHORS
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                                                                                                                                                                                                                             75 ctatttattaactaaccatctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                                                                                                  15 atggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctg 74
                                                                                                                                                                                                                                                                                                                         68;
                                                                                                     166076 bp DNA linear HTG 21-JUL-200 Homo sapiens chromosome 11 clone RP11-348A20 map 11, WORKING DRAFT SEQUENCE, 18 unordered pieces. AC090587
            Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 166076)
                                                                              AC090587.3 GI:14971229
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
  Birren,B.,
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139431. 162043
/note="assembly_name:Contig32"
35428 c 35430 g 43508 t
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89907. .103817
/note="assembly_name:Contig29"
103918. .117239
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77173. .89806
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117340. .139330
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50550. .56392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_name:Contig13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="assembly_name:Contig16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="assembly_name:Contig15
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                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                     Score 45.8; DB Pred. No. 0.002;
  Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                         Mismatches
                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                         37;
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                                                                                                                                                                                                                                                                                                                                                                                                        2297 others
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FEATURES

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Direct Submission

Submitted (03-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 20, 2001 this sequence version replaced gi:14210549.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rleback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
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Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces
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Insert size: 164376; sum-of-contigs
Quality coverage: 8.2 in Q20 bases; agarose-fp
Quality coverage: 8.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: Plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 160051 bases at least Q40 Consensus quality: 162378 bases at least Q30 consensus quality: 163489 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: 348_A_20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
                  13686 13785: gap of 100 bp
13786 16872: contig of 3087 bp in length
                                                                                                  11857 11956:
11957 136
                                                                                                                                                                    10151 10250:
10251 118
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8434 101
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6965 83
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5809 68
16972:
                                                                            5708: contig of 5708 bp in length 5808: gap of 100 bp 6864: gap of 100 bp in length 6964: gap of 106 bp in length 833: contig of 1369 bp in length 10150: contig of 1717 bp in length 10250: gap of 100 bp 10250: gap of 100 bp 11856: contig of 1606 bp in length 11956: gap of 100 bp 11856: contig of 1729 bp in length 113685: contig of 1729 bp in length
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                                                                                       BASE COUNT
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64814 72676: contig of 7863 bp in length
72677 72776: gap of 100 bp
72777 87626: contig of 14850 bp in length
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20147 20246: gap of 100 bp
20247 53285: contig of 33039 bp in length
53286 53385: gap of 100 bp
53386 56431: contig of 3046 bp in length
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                                                                            vector_side:right"
36452 c 36434 g 44341 t
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                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
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87727. .102250
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13786. .16872
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56532. .64713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_end:SP6
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/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="11"
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                                                                                1714 others
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COMMENT

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 atggcatagaaagagcaggaccttgggagcaagaatatctaagtttaattcctgactctg 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 166496)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barran,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,i., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on MAY 27, 2001 this sequence version replaced g1:13270673.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 11 clone RP11-258P13 map 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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Sequencing vector: Plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.960731 consensus quality: 163137 bases at least Q40 consensus quality: 16434 bases at least Q30 consensus quality: 165423 bases at least Q20
                                                                                                                                                                                                                                                                Center project Information
                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                     Center clone name: 258_P_13
                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens chromosome 11, clone RP11-258P13
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Pred. No. 0.002;
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FEATURES
                                                                                                                                                                                         Db 138202 ATGTGGTAGAAAGCACATAAACTCTGGCGCCAGACAAACTAAGGTCAAATCCTGATTTTG 138261
                                                                                                        Db 138262 CTATTTCCTAGCTGTGTAACCCTGAAAAAATTGCTTAACCTCTGT 138306
                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
LOCUS
               AL133413/c
                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                              75 ctatttattaactaaccatctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                                                                                                                   Local
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AL133413
                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         runs of \bar{N}, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                              47782 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 59536: contig of 59536 bp in length 59537 59636: gap of 100 bp 59637 60985: contig of 1349 bp in length 60986 61085: gap of 100 bp 61086 64549: contig of 3464 bp in length 64550 64649: gap of 100 bp 64650 73577 73676: contig of 8927 bp in length 73577 73676: gap of 100 bp 73677 118290: contig of 44614 bp in length
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Insert size: 165896; sum-of-contigs
Quality coverage: 8.3 in Q20 bases;
Quality coverage: 8.4 in Q20 bases;
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118391 165497: contig of 47107 bp in length
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165598 166496; contig of 899
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165598. .166496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_end:T7
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64650. .73576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
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157790 bp
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DEFINITION

Human DNA sequence from clone

RP11-54K22 on chromosome

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RPI1-54K22 is from the library RPCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

EM: EMBL; SW:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human was generated from part of bacterial clone contigs of human as the sequence was generated from part of bacterial clone contigs of human and the sequence was generated from part of bacterial clone contigs of human and the sequence was generated from part of bacterial clone contigs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 11, 2000 this sequence version replaced gi:6966862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3) pseudogene, STSs and AL133413 AL133413.5 GI:6967346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VECTOR: pBACe3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1, (bases 1 to 157790)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                         /note="MIR repeat: 2127. .2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match: GSS: Em:AQ083232
match: STS: Em:G53956"
                                                        'note="MIR repeat: matches 45. .112 of consensus"
                                                                                                           /note="MIR repeat:
                                                                                                                                        /note="MIR repeat: matches 2. .120 of consensus"
2368. .2510
                                                                                                                                                                                                                                                                    /note="MIR repeat: matches 56.
                                                                                                                                                                                                                                                                                                                       note="match: GSS: Em:B85038"
                                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: Em:B89369"
                                                                                                                                                                                                                                                                                                                                                                                                                          note-"match: GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="q34.11-34.2"
/clone="RP11-54K22"
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/chromosome="9"
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                                                                                     .2919
        repeat: matches 6140.
                                                                                                           matches 14.
                                                                                                                                                                                                              matches 209. .253 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                          Em: B86764"
                                                                                                           .162
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                                                                                                        24953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match:
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                                                                                                                                                                                                           3558.
                                                                                                                                                                                                                                   'note="AluSx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18901. .19479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1MD2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="match:
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                                                                                                                                                                                                         .24418
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complement(17541. .18049)
/note="match: GSS: Em:AQ677358"
complement(17569. .17902)
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/note="L1MD repeat: matches -1.
10112. .10338
                                                                                                                                                                                                                                                                            /note="20 copies 2 mer tg 100% conserved"
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/note="L1MD2 repeat: matches 5842.
18472. .18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13953. .14420
/note="LTR38 repeat: matches 86. .556 of consensus"
                                                                                             'note="MER1A repeat: matches 4.
                                                                                                                                       note="L1ME1 repeat: matches 5252. .6163 of consensus"
                                                                                                                                                                                                                                       note="match: GSS: Em:AQ373886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MERIB repeat: matches 1. .336 of consensus"
18808. .18903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3096. .3492
'notce"LLM3 repeat: matches 5112. .5529 of consensus"
3800. .3904
/notce"L2 repeat: matches 2393. .2490 of consensus"
                                                                                                                                                                                                                                                                                                                             'note="AluSq repeat: matches 1. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                               'note="match: GSS:
1370. .21677
                                                                                                                                                                                                                                                                                                                                                                                                                               note="match: GSS: Em:AQ314497"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="match: GSS: 21042. .21464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1ME3A repeat: matches 5285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER45 repeat: matches 1. .178 of consensus"
13830. .13915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="match: GSS: Em:AQ580536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="LTR16C repeat: matches 208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MLT1C repeat: matches 268. .421 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="LTR38 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="Aluyb8 repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MER2 repeat: matches 89. .335 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="L1MB7 repeat: matches
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                        LAME1 repeat: matches 4904. .5252 of consensus" 25670
  repeat: matches 1781.
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                                                                                                                                                                                        repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Em: AQ679820"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Em: AQ177739"
                                                                                                                                                                                                                                                                  22742)
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.1927 of consensus"
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                                                                                                                                                                                                    aggggaagggggtatggcatagaaagagcaggaccttgggagcaagaatatctaagttta 61
                                                                                                                                                                                                                                                                                        AGAAGATGTGGACAGAGCACAGTAAGAGTGTATGCTTTGGAGCCAGGCTTACTCAGTTTTG 84208
Human DNA sequence from clone RP1-68P15 Contains ESTs, STSs and GSSs, complete AL390768.1 GI:9581737
                                                                                           AL390768
                                                                                                                                                                                                                                                                                                                                                                               Conservative
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/note="L2 repeat: matches 2691.
complement(29115. .29540)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 5. .212 complement(32208. .32709)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MER47A repeat: matches 2.
complement(39672. .40087)
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34293. .34585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="27 copies 2 mer aa 85% conserved"
33369. .33427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L2 repeat: matches 2157. .2379 of consensus"
35808. .36027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="LIMC1 repeat: matches 6164 .6322 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="match: GSS: Em:AQ400397"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="match: GSS: Em:AQ432498"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            te="MIR repeat: matches 20. .262 of consensus"
92. .39075
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                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 44.8; DB Pred. No. 0.004;
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                                                                                           57449 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Em: AQ123877"
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                                                                                           DNA
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                                                                  on chromosome 11p13-14.
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During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 57449) Hall,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RP1-68P15 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP5-1137017 is at 57350 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep RPI-68PI5 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotated human repeat sequence elements (e.g. \mathrm{Alu}). Whe sequence is ambiguous, there is an annotation using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence. The true right end of clone XX-SRL9A13 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              teature key
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                                                                                                                                      /note="AluJb repeat: matches 82.
4502. .4569
                                                                                                                                                                                                                           /note="AluJb repeat: matches 1. .301 of consensus"
3516. .4011
                                                                                                                                                                                                                                                                                                                    2858
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/note="AluJo repeat: matches 121.
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/clone="RP1-68P15"
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/db_xref="taxon:9606"
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                                                    11168.
                                                                                                                                                                                                      /note="HAL1 repeat: matches 551.
                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 5. .241 of consensus"
                                                                                                                                                                                                                                                                                                                               2426. .2552
/note="HAL1 repeat: matches 11. .135 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                        'note="MER3 repeat: matches 2. .205 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="match: GSS: Em:AQ244277"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ278896"
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                                                                                                               note="34 copies 2 mer ga 69% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 634
                                                                                               .10960
                           MLT1A2 repeat: matches 1.
                                                                      L1PA2 repeat: matches 395.
                             .114 of consensus"
                                                                                                                                                               .303 of consensus"
                                                                                                                                                                                                        .1073 of consensus
                                                                                                                                                                                                                                                                                                                                                                                    .287 of consensus
                                                                           .6141 of consensus"
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                                                                                                34805
                      /note="LIPA2 repeat: matches 6167. .6240 of consensus"
35046. .41168
/note="IIPA2 repeat: matches 2. .6144 of consensus"
                                                                                                                                                                                                                                                        31947. .33134
/note="L2 repeat: matches 1366. .2713 of consensus"
                                                                                                                                             /note="L1MA10 repeat: matches 6240. .6319 of consensus"
33537. .34804
                                                                                                                                                                                                             complement(32984, .33714)
/note="match: GSS: Em:AQ377120"
                                                                                                                                                                                                                                                                                                                                     /note="MER1A repeat: matches 1.
31376. .31910
                                                                                                                                                                                                                                                                                                                                                                                      /note="LIMA9 repeat: matches 5959. .6303 of consensus" 30869. .31357
                                                                                              /note="HSMAR2 repeat: matches 1. .1300 of consensus"
34805. .34877
                                                                                                                                                                                                                                                                                                    /note="MLT2D repeat: matches 42. .553 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSp repeat: matches 1.
complement(25341. .25695)
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/note="AluSx repeat: matches 1. .312 of consensus"
16352. 17086
/note="LIPA16 repeat: matches 4252. .4960 of consensus"
17079. .17509
/note="match: GSS: Em:AQO79766"
17089. .17465
/note="match: accordance of the consensus"
/note="TIGGER1 repeat: matches 1950. .2359 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluJb repeat: matches 1..309 of consensus"
14364..14376
/note="LIPAL6 repeat: matches 6081..6093 of consensus"
14377..14687
/note="Alusx repeat: matches 1..301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER7A repeat: matches 1..292 of consensus"
24400..24489
/note="45 copies 2 mer ta 66% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14688. .15421
/note="L1PA16 repeat: matches 5329. .6081 of consensus"
15422. .15678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"MLTIA2 repeat: matches 9. .374 of consensus
11771. .11884
/note-"MLTIA2-internal repeat: matches 1. .113 of
consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS: Em:B40764"
26535. .26614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: GSS: Em:B03931"
23411. .23714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1PA2 repeat: matches 4493. .6146 of consensus"
21580. .21989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluSg repeat: matches 1, .293 of consensus"
19121, .20765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSp repeat: matches 1. .185 of consensus"
18784. .19104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSx repeat: matches 8. .289 of consensus"
15679. .16039
.note="LIPA16 repeat: matches 4960. .5329 of consensus"
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11392. .11770
                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MIR repeat: matches 32. .112 of consensus" 0408. .30779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSx repeat: matches 1. .302 of consensus"
24111. .24395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13993. .14056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="TIGGER1 repeat: matches 771. .1964 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Limel repeat: matches 5964. .6164 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="AluJo repeat: matches 1. .289 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 25559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .14363
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                   repeat: matches 2. .6144 of consensus'
                                                                                                                                                                                                                                                                                                                                                        .527 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .299 of
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RESULT 13
AL136384/c
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    ACCESSION
                                            DEFINITION
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Best Local Similarity
                                                                                                                                                             3001 ACTTTGCGACCTTGGACAAGTTAATTAACCTTTGT 2967
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                                                                                                                                                                                  85 actaaccatctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                                                                             ALLISTS 4 172516 bp DNA linear HTG 26-JUL-2000 Homo sapiens chromosome 11 clone RP1-68P15 map p13-14.2, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
ALLISTS 4
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1 rer-
46547
                                                                                                                                                                                                                                                                                                                                                                                               /note="L2 repeat: matches 2042. .2191 of consensus" 51492. .51812 /note="AluYa8 repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              51044. .51354
/note="AluYa8 repeat: matches 1. .309 of consensus"
51364. .51491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1ME1 : 50712. .51086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49824. .49884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSx repeat: matches 3. .311 of consensus"
48839. .49096
/note="LLME1 repeat: matches 5569. .5834 of consensus"
49147. .49207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MSTA
47708. .485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: GSS: Em:AQ789501" 45717. .45996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1MEc repeat: matches 1580. .2001 of consensus" 41590. .41864
/note="Alux repeat: matches 30. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1ME1 repeat: matches 4648. .5569 of consensus"
48530. .48838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46547. .46703
/note="L1ME1 repeat: matches 3983. .4145 of consensus"
47012. .47330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluYb8 repeat: matches 1, 46098. .46235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: STS: Em:G60437"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluJb repeat: matches 6. .287 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44654.
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note="25 copies 2 mer ca 74% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L1ME1 repeat: matches 5833. .6099 of consensus"
19539. .49823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MER2 repeat: matches 25. .84 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="LlME1 repeat: matches 4320. .4648 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L1M4 repeat: matches 3517. .3671 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44654. .44851
/note="match: GSS: Em:AQ451420"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="FLAM_C repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="43 copies 2 mer aa 62% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="LIMEc repeat: matches 283.
                                                                                                                                                                                                                                                                                                                                         36.5%;
66.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 3572. .3761 of
                                                                                                                                                                                                                                                                                                                      Score 43.8; DB 9; Length 57449;
Pred. No. 0.0084;
0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 1. .426 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 6099. .6155 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .297 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consensus"
                                                                                                                                                                                                                                                                                                                      Gaps
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SOURCE ORGANISM

Homo sapiens

VERSION KEYWORDS

AL136384.8 GI:9542701 HTG; HTGS\_PHASE1; HTGS\_DRAFT.

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FEATURES
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DEFINITION
                                            HS37J18/c
                                                                    RESULT
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TITLE
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                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                            97986 AAGAGGATGAGCTACAGAGCAAGACTTTCCAAACTCAAGTCCTGGGTCTGCTACTTAATT 97927
                                                                                                                                     97926 ACTTTGCGACCTTGGACAAGTTAATTAACCTTTGT 97892
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                                                                                                                                                                             85 actaaccatctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator ABI; 0% of reads Chemistry: Dye-terminator Big Dye; 99% of reads Consensus quality: 155580 bases at least 040 Consensus quality: 155880 bases at least 030 Consensus quality: 155942 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 172416; sum-of-contigs
Insert size: 150759; 12.6% error; agarose-fp
Quality coverage: 0.00x in Q20 bases; sum-of-contigs Quality
coverage: 0.00x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 27, 2000 this sequence version replaced gi:9501161.
                                                                                                                                                                                                                                                                                                                      63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: dJ68P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.sauyer.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hall, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 172516)
Human DNA sequence from clone
                       HS37J18
                                                                                                                                                                                                                                                                                                                                                                                                                                                       56528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence: It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved
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16401 17251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="11"
/map="p13-14.2"
/clone="RP1-68P15"
/clone_lib="RPCI-1"
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16401. .172516
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1 172516: contig of 156116 bp in length.
Location/Qualifiers
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30286 c 30207 g 55395 t 10
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    Summary Statistics

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66.3%;
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Pred. No. 0.0078;
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                                                                                                                                                                                                                                                                                                                   Mismatches
37J18 on chromosome 1p36.2-36.3.
                       DNA
                                                                                                                                                                                                                                                                                                                                                         DB 2;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Dec 2, 1998 this sequence version replaced gi:3925562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chrl
37J18 is from the library RPCII constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
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1. (bases 1 to 131427)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2
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Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was generated from part of bacterial clone contigs human chromosome 1, constructed by the Sanger Centre Chromosome
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/chromosome="1"
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/note="MLT1B repeat: matches 1. .381 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 141. .210 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="27 copies 24 mer 79% conserved"
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                                                    /note="MIR repeat: matches 53. .144 of consensus"
                                                                                                                                                                                                                                                                                                                       /note="14 copies 20 mer 58% conserved"
                                                                                                                                                                                                                                                                                                                                                                            /note="AluSx repeat: matches 1. .294 of consensus"
                                                                                                       note="28 copies 2 mer tt 79% conserved"
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.1168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "9 copies 66 mer 82% conserved"
.1613
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                                                                                                                                                                                                                                                                  .41 copies 2 mer cc 57% conserved"
                                                                                                                                                                                                              copies 37 mer 79% conserved"
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                                                                                                                                                                                                                                                                                       /note="5 copies 70 mer 93% conserved"
15459. .15668
/note="6 copies 35 mer 91% conserved"
15681. .15827
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                      19100. .19140
/note="MLT1E repeat: matches 72. .112 of consensus"
19854. .19922
                                                                                                                                                                                                                                                                                                                                                                                           /note="Forced join in tandem repeat; gap clones and PAC PCR to be 1-200bp"
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  /note="MIR repeat: matches 87.
                                                                                                                                      /note="MER77 repeat: matches 5.
18532. .18555
                                                                                                                                                                                                                    /note="MLT1D repeat: matches 1.
16463. .16529
                                                                                                                                                                                                                                                                       /note="L2 repeat: matches 2538. .2685 of consensus"
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8477. .8512
/note="12 copies 3 mer taa 83% conserved"
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/note="LIMB7 repeat: matches 5847. .6143 of consensus" 6535. .6856
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/note="LIMB7 repeat: matches 5654. .5862 of consensus"
6060. .6116
/note="Charliel repeat: matches 2407. .2463 of consensus"
                                                                           note="MLT1E repeat: matches 249.
                                                                                                                                                                                             note="L2 repeat: matches 2413.
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/note="71 copies 7 mer gctgtgt 90% conserved" 14747..15236
/note="7 copies 70 mer 91% conserved"
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15124. .15428
"note="Tandem repeat; poor quality data
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/note="AluSx repeat: matches 132. .289 of consensus"
10990. .11231
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note="3 copies 37 mer 78% conserved"
.5230. .15684
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(4748. 15237
'note="114 copies 35 mer 90% conserved"
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'note="12 repeat: matches 2359.
12285. .12575
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/note="AluSx repeat: matches 6. .132 of consensus"
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/note="11194 repeat: matches 5288. .5414 of consensus"
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/note="Charliel repeat: matches 2146. .2458
                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="5 copies 91 mer 92% conserved"
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4049. .14489
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                                                                                                 6 copies 4 mer aatg 100% conserved" .19007
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.163 of consensus"
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                                                                                     82 ttaactaaccatctttgccaatgttgcttaagcttttt 119
                                                                                                                                                                                                      a 36.3%;
Similarity 65.3%;
54; Conservative
                                                                                                                                                                                                                                                                     /note="L1ME3 repeat: matches 5937. .6164 30493. .30540 /note="3 copies 16 mer 88% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="7 con
29692
                                                                                                                                                                                                                                                                                                                                                           /note="L1PA5 repeat: matches 5943. .6042 of 29872. .29911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /...uue="5 copies 24 mer 70% conserved" 29057. .29147 //note="7 copies 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="2 copies 66 mer 83% conserved"
29040. .29119
/note="5 copies 16 mer 73% conserved"
29048. .29167
/note="5 copies 24 mer 70% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="7 copies 13 mer 69% conserved"
29072. .29151
/note="20 copies 4 mer aaat 66% conserved"
29200. .29504
                                                                                                                                                                                                                                                                                                                                            /note="20 copies 2 mer aa 80% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(25095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22083. .22359
/note="L2_repeat: matches 2416. .2710 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="2 copies 70 mer 84% conserved"
29037. .29168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MER70A repeat: matches 127. .545 of consensus"
complement(25095. .25545)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MER53 repeat: matches 128. .187 of consensus"
20239. .20321
                                                                                                                                                                                                                                                                                                                                                                                           note="18 copies 2 mer ta 81% conserved"
19766 . 29865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26856. .27160

/note="AluSg repeat: matches 1.

27460. .27770

/note="AluSg repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: GSS AQ192529"
26500. .26778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MER53 repeat: matches 94. .182 of consensus"
20256. .20337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluSq repeat: matches 1. .304 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="AluSx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MIR repeat: matches 13. .126 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="L2 repeat: matches 2638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER63A repeat: matches 42. .208 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER53 repeat: matches 1. .89 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                               "7 copies 16 mer 69% conserved" .29725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .29175
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                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                      Score 43.6; DB 9;
Pred. No. 0.0091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat: matches 21.
                                                                                                                                                                                                      34;
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                                                                                                                                                                                                                                      Length 131427;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2747 of
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ACCESSION VERSION

DEFINITION

Homo sapiens chromosome 1 clone SEQUENCE, 26 unordered pieces. ACC04798 GI:7885063

RP11-182C20 map 1, DNA

Linear

HTG 17-MAY-2000 WORKING DRAFT

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (22-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 17, 2000 this sequence version replaced gi:7637293.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bouguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Cooke, P., Dearellano, K., Dewar, K., Dewar, K., Diaz, J.S., Cooke, P., Dearellano, K., Dewar, K., Dewar, K., Dewar, K., Diaz, J.S., Cooke, P., Dewar, K., Dewar, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galagan, J., Gardyna, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dodge, S., Domino, M., Doyle, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                    as soon as it is available and the accession number will be preserved. \begin{tabular}{c} \end{tabular}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 157185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 145137 bases at least Q40 Consensus quality: 150882 bases at least Q30 Consensus quality: 153238 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 4.1 in Q20 bases; agarose-fp Quality coverage: 4.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L7596
Center clone name: 182_C_20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
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Insert size: 154685; sum-of-contigs
                                                                                                         1409 1508: gap of
1509 2661: cor
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                                                     2761: gap of
4282: con
        4382: gap
6145:
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                         1408: contig of 1408 bp in
                                                                              of 100 bp
contig of 1153 p
of 100 bp
                                                contig of
        contig
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     100 bp
of 1763
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                                                     00 bp
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bp_in
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length
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137262 137361:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 8312: contig of 2067 bp in le
13 8412: gap of 100 bp
13 10646: contig of 2234 bp in le
17 10746: gap of 100 bp
47 13916: contig of 3170 bp in le
17 14016: gap of 100 bp
17 14016: gap of 2319 bp in le
                                                   19381.
                                                                                                                                                            14017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                            note="assembly_fragment"
                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP11-182C20"
/clone_lib="RPCI-11 Human Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon;9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                        note="assembly_fragment"
                                                                      'note="assembly_fragment"
                                                                                                                         note="assembly_fragment"
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57837: contig of 6195 bp in length

57937: gap of 100 bp

65412: contig of 7475 bp in length
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28217: contig of 4259 bp in
28317: gap of 100 bp
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cont
gap of
23858;
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32600: contig of 4283 bp in length
700: gap of 100 bp
36397: contig of
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108184: contig of 10467 bp in length
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BASE COUNT 40688 a ORIGIN
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Search completed: September 7, 2002, 18:23:45 Job time: 28924 sec

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Title:
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Sequence:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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Email: walbotescantord.edu  Plate: 486039 row: F column: 12.  Location/Qualifiers  1256	FEATURES
Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221	
University Unpublished (1999) Contact: Walbot V Contact: Walbot V	JOURNAL COMMENT
Spermatophyta; Magnollophyta; Lillopsida; Podles; Podcede; PACC clade; Panicoideae; Andropogoneae; Zea.  1 (bases 1 to 256) Walbot, V. Maize ESTs from various cDNA libraries sequenced at Stanford	REFERENCE AUTHORS TITLE
A1629829.1 GI:4681159 EST. Zea mays. Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	VERSION KEYWORDS SOURCE ORGANISM
A1629829 256 bp mRNA linear EST 26-APR-1999 486039F12.x3 486 - leaf primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence.	RESULT 1 AI629829 LOCUS DEFINITION ACCESSION

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                                        AW943206 622 bp mRNA linear EST 23-APR-2001 LD33880.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD33880 3 similar to AC005711: Drosophila melanogaster, chromosome 2L, region 33D3-33E8, BAC clone BACR48M09,
            complete sequence, mRNA sequence AW943206
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855 California Ave, Palo Alto, CA 94304,
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/note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
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libraries 486, 487, 496, 603, 605, 606, 614, 618, 660, 687, 687, 707, and 945. Contigs were assembled using TICR's
CAP program and a representative EST from each contig was
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nes 18; Conser
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                                      Unpublished (2000)
Contact: Robert B.
                                                                                                                        Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                    1 (bases 1 to 714)
Dunn, D., Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                GSS
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University of Utah University of Utah
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                     Mus musculus
                                                                                 plasmid inserts
                                                                                                      Mouse whole genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic AE003636: Drosophila melanogaster genomic scaffold 142000013386055 section 29 of 63, complete sequence.: 03/12/2001
                                                                                                                                                                                                                                                                                             house mouse.
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High quality sequence stop: 423.
Location/Qualifiers
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Other_ESTs: LD33880.5prime
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1 (bases 1 to 622)
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One Cyclotron Rd, Berkeley, CA 94720, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BDGP/HHMI Drosophila EST Project
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/sex="male and female"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
/note="0.rgan: embryo: Vector: p072; Site_1: EcoRI;
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/db_xref="taxon:7227"
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Insert Length: 10000 Std Erro
Plate: 0236 row: O column: 18

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -

                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence SP6 end of BAC BACN04I03 of DrosBAC library from Drosophila melanogaster (fruit
                                                                            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Diptera; Brachyo; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                    Drosophila melanogaster
Eukaryota; Metazoa; Art
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801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[4732114]gb]AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coil XII0(Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0236018"
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                                                                                                                                                                                                                    melanogaster genome using these BACS. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-88 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://www.dathur.org/philabac/htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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AL062157
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755 c 248 g
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                                                         /clone="BACR05E09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
Tel: 81-45-503-9222
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Unpublished (2000)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-44 (1999)
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303.
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                                                                                                                                                                                                                                                                                                                                                                                        details
                                                                                                                                                                                                                                                                                                                                                                                                     visit our web site (http://genome.rtc.riken.go.jp) for
/tissue_type="testis"
/dev_stage="15 days embryo"
/lab_host="DH10B"
                                                                                                                                male testis"
                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="8030453F10"
                                                                                                                                                    /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                       /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                            /sex="male"
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
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Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
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Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
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Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya
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Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
, M., Muramatsu, M. and Hayashizaki, Y.
Unpublished (2000)
                                                                                                                                                                                                                                                       Contact: Yoshihidé Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB559660 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone £330039011 3' similar to U49385 Mus musculus CTP synthetase homolog (CTPsH) mRNA, mRNA sequence.
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Genomic Sciences Center and Genome Science Laboratory
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                 Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-47107.TJ
                                                                                                                                                                                        Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M.,
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                                                                                           Contact: Shaying Zhao
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/dev_stage="2 days pregnant adult"
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                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                               Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                      Contact: Shaying Zhao, William Nierman, Mark Adams
                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Other_GSSs: CITBI-E1-2589J3.TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                              Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                          The Institute for Genomic Research
                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                            Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
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/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

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/clone="RPCI-23-47107"
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/strain="C57BL/6J"
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aaactacctaagagctatct
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                                                                                                                                                                                                                                                                                                                                                                      Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                        18;
                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 For Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
Other_GSSs: AG-ND-12404.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftu Direct Submission of BAC-end sequences from Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H400996
AG-ND-12404.TF ND-TAM Anopheles
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                                                                                                                                                    /db_xref="taxon:7165"
/clone="AG-ND-12404"
/clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
93 c 65 g 107 t
                                                                                                                                                                                                                                                    /organism="Anopheles gambiae"
/strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI; CalTech Human BAC Library D" 54 c 64 g 168 t 1 others
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/clone="2589J3"
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90.0%;
                                Score 16.8; DB 12,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 540)
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                                                             Homo sapiens
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Contact: Michalek W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL509860 Hordeum vulgare Barke developing caryopsis (3 Hordeum vulgare cDNA clone HY03B17u 3', mRNA sequence.
                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: Ml3uni primer for 3'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute for Plant Genetics and Crop Plant Research Corrensstr. 3, D-06466 Gatersleben, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contains less than two ambiguities. The maximum length was set to 700\ \mathrm{bp}^{\mathrm{m}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', 'a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window
                                                                                                                          GI:2929136
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/lab_host="XLOLR"
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(3.-15.DAP)"
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/db_xref="taxon:4513"
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90.0%;
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Pred. No. 5.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 576)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                       GSS
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Seq primer: SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
Other_GSSs: RPCI11-16C24.TP RPCI11-16C24.TVB
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Use of BAC End Sequences for Sequence-Ready Map Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
                                                                                                                                         Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ483186.1 GI:10646948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ483186
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                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                              University of Utah
University of Utah
Rm. 308, Biomedical
                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb
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ddunn@genetics.utah.edu
                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCIII Human Male BAC Library"
104 c 106 g 143 t
                                                                          Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
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/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                         Genome Center
                                                                                Polymers Research Bldg
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Pred. No. 5.9e+02;
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AUTHORS
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                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV834315 K. Sato unpublished cDNA library: vulgare shoots germination Hordeum vulgare
                                                                 Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
URL:http://www.rib.okayama-u.ac.jp/barley/
                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare subsp. vulgare.
Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 10000 Plate: 0308 row: N
                                                                                                                                                                                                               Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV834315.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV834315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone rbags14a02, mRNA sequence.
                                                    Sato, K.,
                                                                                                                                                                                         Contact: Kazuhiro Sato
database:http://www.shigen.nig.ac.jp/barley/Barley.html.
                         submission;
                                                                                                                                                                                                                                   Barley EST sequencing project in NIG and Okayama Univ
                                                                                                                                                                                                                                                                 Sato,
                                                                                                                                                                                                                                                                                                                 Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                        (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                               Saisho,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:14526404
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90.0%;
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                                                    and Kohara, Y. Direct
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FEATURES

Source

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/organisms"Hordeum vulgare subsp. vulgare"
/cultivar="Haruna Nijo"
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/db_xref="Haruna Nijo"
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/tissue_type="shoots"
/dev_stage="germination"
/dev_stage="g
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Result
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Listing first 45 summaries
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                      Score
 seq length: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aaactacctaagagctatct 20
                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
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                                    7557675711777577677666
         US-10-035-832-1262

US-10-035-832-1349

US-10-028-754-258416

US-10-027-632-258417

US-10-028-754-11812

US-10-028-753-111702

US-10-027-632-111703

US-09-721-544-17137

US-10-027-632-50683

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US-10-027-632-50684

US-10-027-632-50684

US-10-027-632-50684

US-10-027-632-50685

US-10-10-124-805-67

US-10-124-805-67

US-09-705-2568-1146

US-10-108-846-9873

US-10-198-846-9873

US-10-198-846-9873

US-10-198-846-9873

US-10-198-846-9873

US-10-198-846-9873

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US-10-27-632-11325

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US-10-27-632-1167
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                                 Sequence 1262, Ap
Sequence 5310, Ap
Sequence 258416,
Sequence 258417,
Sequence 11812,
Sequence 111702,
Sequence 1171703,
Sequence 17137, A
Sequence 50683, A
Sequence 50684, A
Sequence 50685, A
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 1146, Ap
Sequence 178902,
Sequence 178902,
Sequence 178902,
Sequence 178902,
Sequence 11325, Ap
Sequence 11325, Ap
Sequence 11325, Ap
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Sequence Sequence Sequence Sequence Sequence

2106, Ap 2167, Ap 2148, Ap

RESULT 2 US-10-035-832-1349 Sequence 1349, Application US/10035832 GENERAL INFORMATION: APPLICANT: Engelhard, Eric FILE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER FILE REFERENCE: A-71249/RMS/DCF CURRENT APPLICATION NUMBER: US/10/035,832 CURRENT FILING DATE: 2002-07-22 PRIOR APPLICATION NUMBER: US 09/747,377 PRIOR FILING DATE: 2000-12-22 PRIOR FILING DATE: 2001-03-02 PRIOR FILING DATE: 2001-03-02 NUMBER OF SEQ ID NOS: 1613 SOFTWARE: Patentin version 3.1	Query Match 100.0%; Score 20; DB 6; Length 45121; Best Local Similarity 100.0%; Pred. No. 0.89; Matches 20; Conservative 0; Mismatches 0; Indels 0; Qy 1 aaactacctaagagctatct 20	RESULT 1 US-10-035-832-1262 ; Sequence 1262, Application US/10035832 ; GENERAL INFORMATION: APPLICANT: MOTTIS, DAVId : APPLICANT: MOTTIS, DAVId : APPLICANT: Engelhard, Eric : TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER : FILE REFERENCE: A-71249/RMS/DCF : CURRENT FILING DATE: 2002-07-22 : PRIOR APPLICATION NUMBER: US/10/035,832 : CURRENT APPLICATION NUMBER: US 09/747,377 : PRIOR FILING DATE: 2000-12-22 : PRIOR APPLICATION NUMBER: US 09/747,377 : PRIOR FILING DATE: 2001-03-02 : NUMBER OF ESQ ID NOS: 1613 : SOFTWARE: PatentIn version 3.1 : SEQ ID NO 1262 : LENGTH: 45121 : TYPE: DNA : ORGANISM: Homo sapiens US-10-035-832-1262	ALIGNMENTS	c         26         15.2         76.0         498         6         US-10-182-997-2121         Sequence           c         27         15.2         76.0         498         6         US-10-203-135-2064         Sequence           c         28         15.2         76.0         498         6         US-10-203-137-2220         Sequence           c         29         15.2         76.0         498         6         US-10-203-137-2220         Sequence           c         30         15.2         76.0         498         6         US-10-207-632-20673         Sequence           c         31         15.2         76.0         498         7         US-10-207-632-226676         Sequence           c         31         15.2         76.0         637         7         US-10-207-632-226676         Sequence           c         33         15.2         76.0         915         7         US-10-207-632-226676         Sequence           c         34         15.2         76.0         915         7         US-10-207-632-120073         Sequence           c         35         15.2         76.0         1045         7         US-10-207-632-120073         Sequence
CANCER	45121; ls 0	DANCER		Sequence 2121, Apsequence 2092, Apsequence 2220, Appsequence 2197, Apsequence 21167, Appsequence 21676, Sequence 21676, Sequence 210073, Sequence 119014, Sequence 201020, Sequence 677, Appsequence 678, Appsequence 679, Appsequence 678, Appseque
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SEQ ID NO 1349

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; LOCATION: (95348)..(95367)
; OTHER INFORMATION: "n" at positions 95348 thru 95367
US-10-035-832-1349
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                                                                   Query Match
Best Local Similarity
                                                        Matches
22555 aaactacctaaaagctatc 22573
                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (91740)..(91802)
OTHER_INFORMATION: "n" at positions
                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (84883)..(84902)
OTHER INFORMATION: "n" at positions
                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (67304)...(67872)
OTHER INFORMATION: "n" at
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (66416)..(66549)
OTHER INFORMATION: "n" at positions 66416 thru
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: (63327)..(63350) OTHER INFORMATION: "n" at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (58367)..(58386)
OTHER INFORMATION: "n" at
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NAME/KEY: misc_feature
LOCATION: (4902)..(4921)
OTHER INFORMATION: "n" at positions
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LOCATION: (56214)..(56713)
OTHER INFORMATION: "n" at positions 56214 thru 56713
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LOCATION: (51928)..(51947)
OTHER INFORMATION: "n" at positions 51928 thru
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LOCATION: (36676)..(36765)
OTHER INFORMATION: "n" at positions
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LOCATION: (12187)..(12206)
OTHER INFORMATION: "n" at positions 12187 thru 12206
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LOCATION: (7901)..(8020)
OTHER INFORMATION: "n" at positions 7901 thru
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             l aaactacctaagagctatc 19
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                                                     Conservative
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94.7%;
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                                                                 Score 17.4;
Pred. No. 2
                                                    ed. No. 27;
Mismatches
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RESULT 3

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902 aaactacctaagatccatct 921

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CURRENT APPLICATION NUMBER: US/10/098,754
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 09/791539
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 21107
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5310
ELNGTH: 461
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-754-5310
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                                                                                                                                                   ; ORGANISM: Human US-10-027-632-258416
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SEQ ID NO 258416
LENGTH: 1022
                                                         Matches
                                                                       Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: 060/185,218 PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
FILE REFERENCE: ATX-001CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Harrington, John J
APPLICANT: Jackson, P. David
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                                                                                                                                                                                         TYPE: DNA
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1 aaactacctaagagctatct 20
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                                                       18;
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                                                       Conservative
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                                                                       84.0%;
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90.0%;
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Pred. No. 26
                                                                       Score 16.8;
Pred. No. 3
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                         30;
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                                                                                       Length 1022;
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                                                   Gaps
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-258417
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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ORGANISM: Homo sapiens
FEATURE:
FAME/KEY: misc_feature
LOCATION: (1)...(1223)
OTHER INFORMATION: n = A,T,C or G
US-10-098-754-11812
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

FILE REFERENCE: 108827.129
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 09/791539
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ramachandran, Rakesh
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
FILE REFERENCE: ATX-001CN
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                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-02-
NUMBER OF SEQ ID NOS: 21107
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                                                                                                                                       TYPE: DNA
                                                                                                                                                             LENGTH: 1223
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Cain, Scott
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Pred. No. 3
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US-10-027-632-111702
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1909-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-027-632-111703
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                                                                                                                                                                                                                                                                                                                                  Sequence 111703, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 111702
LENGTH: 2500
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Best Local Similarity
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 108827.
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90.0%; Pred. No. 30;
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Pred. No. 34;
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APPLICANT: Verná, Ron

APPLICANT: Yang, Fei

FITTE OF INVENTION: Novel Nucleic Acid Sequences Obtained

TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained

TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained

FILE REFERENCE: 728C1P

CURRENT APPLICATION NUMBER: US/09/721,544

CURRENT FILING DATE: 19000-11-21

PRIOR APPLICATION NUMBER: 09/515,128

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: 09/534,341

PRIOR APPLICATION NUMBER: 09/034,341

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 24489

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 337

TYPE: DATA
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 111703
LENGTH: 2500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1358 aaactgcctaagagccatct 1377
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Faulkner, Brandy
Garcia, Veronica
Giedt, Gretchen
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Dickson, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith, Benjamin
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Lomelli, Michelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jessen, Aaron
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                                                Conservative
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                                                                    79.0%;
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90.0%; Pred. No. 34;
                                         0; Mismatches
                                                                 Score 15.8;
Pred. No. 89
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                                         2
                                                                                  Length 337;
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                                    Gaps
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                                           PRIOR FILING DATE: 1000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
NUMBER: US 60/146,002
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US-10-027-632-50683
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827,129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006
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GENERAL INFORMATION:
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       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR ETILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR ETLING DATE: 1999-08-09
PRIOR ETLING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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TYPE: DNA
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FastSEQ for Windows Version 4.0
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Pred. No. 9
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US-09-721-544-17137/c; Sequence 17137, App.; GENERAL INFORMATION

APPLICANT:

APPLICANT: APPLICANT: APPLICANT:

APPLICANT: APPLICANT:

Drake,

Jim

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US-10-027-632-111703

TYPE: DNA ORGANISM: Human

Query Match
Best Local Similarity

Matches

; ORGANISM: Homo sapiens US-09-721-544-17137

TYPE: DNA

APPLICANT:

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Tkach, Joe Tran, Lien

Raisi, Fariba

APPLICANT:

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Kita, David

Гее

labat, Ivan

Hunter, Kelly

Query Match Best Local Similarity Matches 17; Conserv

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В
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; ORGANISM: Human
US-10-027-632-50683
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PRIOR PRIOR DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                 Sequence 50685, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108877.129
FILE REFERENCE: 108877.129
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LENGTH: 498
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 498
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res 17; Conservation
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Local Similarity 89.5%;
hes 17; Conservative
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Pred. No. 94
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US-10-124-805-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US02-12378-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 50685
LENGTH: 498
TYPE: DNA
                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 627
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
                                                                           Matches
                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: PCT/US02/12378
CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Durham, Margarita
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.47003PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR EILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Houghton, Raymond L.
                                                                                                                                                                                                       LENGTH: 1022
TYPE: DNA
                                                                                                                                                                                    ORGANISM: Homo sapiens
539 acctacctaatagctatct 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 aactacctaagagctatct 20
| ||||||||||||| |||
473 agctacctaagagctttct 491
                   2 aactacctaagagctatct 20
                                                                         17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Fanger, Gary R. Vedvick, Thomas S. McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Persing, David H. Jiang, Yuqiu Dillon, Davin C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepler, William T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harlocker, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitcham, Jennifer L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sleath, Paul
                                                                                         79.0%;
89.5%;
                                                                         Score 15.8; DB 1; Length 1022; Pred. No. 1e+02; 0; Mismatches 2; Indels 0
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                                                                     Gaps
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Sequence 67, Application US/10124805 GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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В
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                                                                    Pending_Patents_NA_Main: *
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen
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31.271 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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922.00	92.00 92.00 92.00	92.0 92.0 92.0 92.0	100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query Match
527 527 637 639	290 290 290 458 458	285 285 5	20 40 40 1608 1608 1608 2165 2165 2380 2380 2827 3212 45121 45121	Length I
53535355	33337 344 344	47 17 33	322 322 322 322 322 322 322 322 322 322	DB
-209-830-52545 -873-402A-3718 -209-830-3718 -873-402A-3631 -209-830-3631 -209-830-3631 -865-439A-7113	US-09-303-031A-7338 US-09-894-949-7338 US-09-894-949A-7338 US-09-865-439A-11835 US-09-306-350A-14682 US-09-306-350A-14682 US-09-909-629-14682	-60-085-147-1327 -09-303-031A-870 -09-894-949-8707 -09-894-949A-870	US-09-834-291-36 US-09-834-291-30 US-08-377-522C-1 US-08-377-522D-1 US-08-377-522D-1 US-09-665-6158-94 US-09-6834-291-3 US-09-834-291-3 US-09-834-291-1 US-09-834-291-1 US-09-834-291-1 US-09-834-291-1 US-09-834-291-1	ID
52545, 3718, A 3718, A 3631, A 3631, A 71133, 115280,	Sequence /338, Ap Sequence 7338, Ap Sequence 7338, Ap Sequence 11835, A Sequence 14682, A Sequence 14682, A Sequence 180806, A	1327, 8707, 8707, 8707,	16, Ap 22, Ap 20, Ap 30, Ap 1, Appl 1, Appl 1, Appl 1, Appl 1, Appl 2, Ap 2, A	Description

```
Sequence 16. Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Willer-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 20
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; ORGANISM: Homo Sapiens
US-09-834-291-16
                                                                                                                 APPLICANT: Muller Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: DCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                      S-09-834 ...
Sequence 22, Appi...
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
AMILER-Schilling, Martina
Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-834-291-16
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Matches
                          SOFTWARE: PatentIn Ver.
SEQ ID NO 22
LENGTH: 40
TYPE: DNA
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Best Local Similarity
ORGANISM: Homo Sapiens
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US-09-684-016-269389

US-09-708-427-74487

US-09-708-427-84689

US-09-708-427-73361

US-60-312-544-2159

US-60-226-326-955

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US-60-191-637-13830

US-60-191-637-13830

US-60-191-637-13830
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Pred. No. 4.3;
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Sequence 74487, A
Sequence 84689, A
Sequence 2159, App
Sequence 955, App
Sequence 13760, A
Sequence 13801, A
Sequence 13801, A
Sequence 11371, A
Sequence 11393, A
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Sequence
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-377-522-1
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PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH AC
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Best Local Similarity
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Best Local :
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDITION OF THE PROPERTY OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Human Fas Gene Promoter Region NUMBER OF SEQUENCES: 2
FILING DATE: 20-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mountz, John D.
APPLICANT: Liu, Changdan
APPLICANT: Cheng, Jianhua
APPLICANT: Koopman, Willia
                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
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Koopman, William J.
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; LOCATION:
US-08-377-522-1
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US-08-377-522C-1
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                              TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 1608 base pairs
TYPE: nucleic acid
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                                                                                                                                                                           NAME: Benjamin Aaron Adler, Ph.D., REGISTON NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919
TELECOMMUNICATION INFORMATION: 777-2321
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/377,522C
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MEDIUM TYPE: 3.5 inch floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mountz et al.
TITLE OF INVENTION: Huma
                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                             SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL:
ANTI-SENSE: r
                               MOLECULE TYPE:
DESCRIPTION:
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                                                                           TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                             LENGTH:
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                               genomic DNA
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100.0%; Pred. No. 8;
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                                                                                                                                                                                                                                                                                                      NAME: Benjamin Aaron Adler, Ph.D., J.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEPHONE: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
            TISSUE TYPE: placental
IMMEDIATE SOURCE:
LIBRARY: (FIXII; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMBL1
POSITION IN GENOME:
FEATURE:
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TISSUE TYPE: placental
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: January CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                       MOLECULE TYPE:
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STREET: ...
TTTY: Houston
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PUBLICATION INFORMATION:
                                                                                                                                                                      ANTI-SENSE:
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CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto
                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/377,522D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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Pred. No. 8;
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; FEATURE;
HAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-802-669-94
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; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-665-615B-94
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GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Wyatt, Jacqueline
TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 94, Application US/09802669 GENERAL INFORMATION:
                                                                                                                             SEQ ID NO 94
                                                                                                                                                                                                        APPLICANT: Wyatt, Jacqueline
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR ETLING DATE: 2000-09-18
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Best Local Similarity
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SEQ ID NO 94
LENGTH: 2165
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Best Local :
                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/290,640 PRIOR FILING DATE: 1999-04-12
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CURRENT APPLICATION NUMBER: US/09/665,615B
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 179
COEMINATE: 1999-04-12
                                                                                                                                              SOFTWARE:
                                                                                                                                                             NUMBER OF SEQ ID NOS: 180
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dean, Nicholas M. APPLICANT: Marcusson, Eric G.
                                                               TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                            LENGTH:
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Pred. No.
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FILE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 4
LENGTH: 2827
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                                                                                                                                                 ; TYPE: DNA; ORGANISM: Homo Sapiens US-09-834-291-4
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SEQ ID NO 3
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-3
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
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                                                         Matches
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                                                                          Best Local Similarity
                                                                                          Query Match
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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                                                       Conservative
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RESULT 12
US-09-997-722-10
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              RESULT 13
US-09-298-328A-1327/c
; Seguence 1327, Application US/09298328A
; GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Engelhard, Eric TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER FILE REFERENCE: A-71171/RMS/DCF
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CURRENT FILING DATE: 2001-11-30
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                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/798,586 PRIOR FILING DATE: 2001-03-02 NUMBER OF SEQ ID NOS: 301
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PRIOR FILING DATE: 2000-12-22
APPLICANT: Lalgudi, Raghunath, V.
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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Oren, Moshe
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US-60-085-147-1327/c
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NAME/KEY: misc_feature
OTHER INFORMATION: Inc:
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TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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PRIOR APPLICATION NUMBER: 60/085,146
PRIOR FILING DATE: May 12, 1998
NUMBER OF SEQ ID NOS: 6550
SOFTWARE: PERL PROGram
SEQ ID NO 1327
TELEFAX: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1327:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 base --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1327, Application US/60085147 GENERAL INFORMATION:
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APPLICANT: Sherman, Bradley, K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN LEAF FILE REFERENCE: PL-0013 US

CURRENT APPLICATION NUMBER: US/09/298,328A

CURRENT FILING DATE: 1999-04-21
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LOCATION: 159
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lalgual, ANGLES APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley
APPLICANTE SHERMAN, BRADLEY
APPLICANT: SHERMAN, BRADLEY
APPLIC
                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 8.0 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 AAACTACCTGAGAGCTATCT 190
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 aaactacctaagagctatct 20
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Pred. No. 42
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RESULT 15
US-09-303-031A-8707/c
; Sequence 8707, Application US/09303031A
; GENERAL INFORMATION:
; APPLICANT: Rashunath, Laigudi
; APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Ito, Laura Y.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN CALLUS
; FILE REFERENCE: PL-0011 US
; CURRENT APPLICATION NUMBER: US/09/303,031A
; CURRENT APPLICATION NUMBER: US/09/303,031A
; CURRENT FILING DATE: 1999-04-29
; PRIOR APPLICATION UNUMBER: 60/084,493
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 9627
; SOFTWARE: PERL Program
; SEQ ID NO 8707
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Zea mays
; EAGURE:
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; CLONE: 700164576H1
US-60-085-147-1327
Search completed: September 7, 2002, 22:31:48 Job time: 43802 sec
                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature; OTHER INFORMATION: Incyte ID No: 700476268H1; NAME/KEY: unsure; LOCATION: 36, 158; OTHER INFORMATION: a, t, c, g, or other US-09-303-031a-8707
                                                                                                                                                          QY
                                                                                                                                                                                                      Query Match 92.0%; Score 18.4; Best Local Similarity 95.0%; Pred. No. 43; Matches 19; Conservative 0; Mismatches
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                                                                                                               189 AMACTACCTGAGAGCTATCT 170
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Dackfiles1.seq:*
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Copyright (c) 1993 - 2000
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US-09-170-996-27
US-07-744-282C-22
US-07-744-282C-24
US-07-744-282C-24
US-08-981-957D-12
US-08-484-105-3
US-09-288-337B-31
US-09-288-337B-31
US-09-288-337B-31
US-09-288-713-557B-30
US-08-713-557B-30
US-08-82-742-9
US-08-492-459-7
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US-08-493-752-5
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US-08-716-873-21
US-09-368-311-21
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                                                                               Sequence 21, Application US/07744282C Patent No. 5521300 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                            Query Match
APPLICANT: Shah, Jyots
APPLICANT: Nietupski,
APPLICANT: Liu, Jing
TITLE OF INVENTION: My
TITLE OF INVENTION: My
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-170-996-27
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 6831 base pairs
                                                                                                                                                                                            6690 AAACTACCTAAGACGTATCT 6709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/609,049
FILING DATE: 29-FEB-1996
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NO. 6291220el PI 3-Kinase Polypeptides NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Molz, Lisa
APPLICANT: Chen, Yen-Wen
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 6831 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                      1 aaactacctaagagctatct 20
                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
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No. 6291220
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                                              Shah, Jyotsna S.
Nietupski, Raymond M.
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                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Oligonucleotides Complementary to Mycobacterial Nucleic Acids
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Pred. No. 3.
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RESULT 4
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APPLICANT: Shah, Jyotsna S.

APPLICANT: Nietupski, Raymond M.

APPLICANT: Liu, Jing

TITLE OF INVENTION: Oligonucleotides Complementary to

TITLE OF INVENTION: Mycobacterial Nucleic Acids

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:

ADDRESSE: Kevin M. Farrell, P.C.
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                         FILING DATE: August 13, 1991 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: GT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,282C
APPLICATION NUMBER: US/07/744,282C
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kevin M. Farrell
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CORRESPONDENCE ADDRESS:
                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                               ZIP: 03911
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REGISTRATION NUMBER:
                  NAME:
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August 13, 1991
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Pred. No. 52;
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US-07-744-282C-24/c
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                                                                                                                                                                                                                         ; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (gen
US-07-744-282C-24
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                                                                                       Matches
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,
EILING DATE: August 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kewin M. Fairell
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: GTR90
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1050881
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LENGTH: 126 base pairs
TYPE: nucleic acid
STRANDEDWESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shah, Jyotsna S.
APPLICANT: Nietupski, Raymond M.
APPLICANT: Liu, Jing
TITLE OF INVENTION: Oligonucleotides Complementary to
TITLE OF INVENTION: Mycobacterial Nucleic Acids
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
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nes 16; Conserv
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                                                                                    Conservative
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- NO: 22:
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80.0%; Pred. No. 52;
tive 0; Mismatches
                                                                                                           71.0%; Score 14.2;
80.0%; Pred. No. 52;
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                                                                                    0;
                                                                                       Mismatches
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                                                                                                                                        Length 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08484105 Patent No. 5589341
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KIY, THOMAS
APPLICANT: SCHULTZ, JOACHIM
APPLICANT: SCHULTZ, JOACHIM
TITLE OF INVENTION: CATHEPSIN-L, ITS PREPRO FORM AND THE CORRESPONDING
TITLE OF INVENTION: PROPEPTIDE FROM CILIATES
FILE REFERENCE: 514426-3595
CURRENT APPLICATION UMBER: US/08/981,957D
CURRENT FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: PCT/EP97/02388
PRIOR FILING DATE: 1997-05-09
PRIOR FILING DATE: 1996-05-14
PRIOR FILING DATE: 196-05-14
NUMBER: OF SEQ. ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Paramecium tetraurelia
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APPLICANT:
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                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                               ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                    CLASSIFICATION: 435
                                                                                                                 FILING DATE
                                                                                                                                              APPLICATION NUMBER:
        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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FOSS, Margit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCNALLY, Francis J
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Pred. No. 69;
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TELEPHONE: (415) 494-8//1
TELEFAX: (415) 494-8//1
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2809 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPOOLOGY: linear
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                                          REFERENCE/DOCKET NUMBER: A-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELEFAX: (415) 494-8771
TELEE: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                     ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
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                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
 STRANDEDNESS:
               TYPE: nucleic acid
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mes 16; Conserv
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                 USA
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HERSKOWITZ, Ira
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FOSS, Margit
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KOBAYASHI, Ryuji
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807..2666
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double
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84.2%;
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Pred. No. 75
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US-09-299-843A-31/c
; Sequence 31, Application US/09299843A
; Patent No. 6107475
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GENERAL INFORMATION:
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
                                                                      FEATURE:
                                                                                                                                                                        SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
                                                                                    MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2539 ATCGACCTTAGAGCTATCT 2521
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                                                                                                       TOPOLOGY:
                                                                                                                                         TYPE:
                                                        NAME/KEY:
                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                   LOCATION:
                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 s
CITY: Chicago
                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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LOCATION:
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                                                                                                                                nucleic acid
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6300 Sears Tower, 233 South Wacker Drive
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807..2666
                                                                                                                   single
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84.2%;
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Pred. No. 75;
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; LOCATION: US-09-299-843A-31
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                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: 31: US-09-088-337B-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31, Application US/09088337B Patent No. 6348574
GENERAL INFORMATION:
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Best Local Similarity
Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2968 AGACTGCCAAAGAGCTATC 2950
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6348574and, Greta E.
REGISTARTION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 aaactacctaagagctatc 19
| ||| || |||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Godiska, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein,
                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                             LENGTH: 3119 base pairs
                                                                                                                                                                                         OCATION:
 Conservative
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94..1158
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84.2%;
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Pred. No. 76;
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               Score 14.2;
Pred. No. 76;
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                                     DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09245041 Patent No. 6274339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/08713557B Patent No. 5912168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY FILE REFERENCE: 7853-136
CURRENT APPLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: 60/093,630
EARLIER APPLICATION NUMBER: 60/093,630
EARLIER FILING DATE: 1998-07-21
EARLIER APPLICATION NUMBER: 60/104,978
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Moore, K. APPLICANT: Nagle, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 90050
TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,557B
FILING DATE: 30-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Watson, James D. APPLICANT: Rudert, Fritz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2968 AGACTGCCAAAGAGCTATC 2950
                                                                                           FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                     NAME: Speckman, Ann W
REGISTRATION NUMBER:
                                                                               FILING DATE:
                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                   STATE:
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   REFERENCE/DOCKET NUMBER:
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2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                     Diskette
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                   31,881
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Pred. No. 1.1e+02;
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         Query Match
Best Local Similarity 88.2
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:
PATOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/844,296
FILING DATE: February 28, 1992
APPLICATION NUMBER: 07/552,216
FILING DATE: February 28, 1991
APPLICATION NUMBER: 1991
APPLICATION: TRACE: 1991
APPLICATION NUMBER: 1991
APPLICATION NUMBER: 1991
                                                                                                                                                                                                                                                             NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                       TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sager, Ruth
TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
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CITY: Boston
STATE: Massac
                                                                                                                                                       STRANDEDNESS:
                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                           LENGTH:
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compress: 225 Franklin Street
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02110-2804
                                                                                                                                                                      nucleic acid
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                                         69.0%;
88.2%;
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                                                                                                                                                                                                                                 9:
                        0; Mismatches
                                         Score 13.8;
Pred. No. 97;
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                                                            DB 1; Length 362;
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                                                                         US-09-073-587-1
Sequence 1, Application US/09073587
Patent No. 6268552
GENERAL INFORMATION:
APPLICANT: Li, Yi
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; ORGANISM:
US-08-998-416-670
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                                                                       Matches
                                                                                        Best Local Similarity
                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 631 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
168 AAAATACCAAAGAGCTA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                        TOPOLOGY:
                1 aaactacctaagagcta 17
                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 AAGCAACCTAAGAGCTA 79
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                                                                     Conservative
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Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mohr, Christine
                                                                                                                                                                               PAG1446UP
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                                                                                                                                                                                                                 DNA (genomic)
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N: 435
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                                                                                      Score 13.8; DB 4; Length 631; Pred. No. 1e+02;
                                                                       Mismatches
                                                                   0;
                                                                Gaps
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NUMBER OF INVENTION: Transgenic Seedless Plants
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORREST 5370 Manhattan Circle, Suite 201
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: LBM PC Compatible
OPERATING SYSTEM: CC.005/NS-DOS
COUNTRY: US
COMPUTER: LBM PC Compatible
OPERATING SYSTEM: US 00/045,725
FILING DATE: 06-MAY-1998
CLASSIFICATION UNMER: US 00/045,725
FILING DATE: 06-MAY-1998
CLASSIFICATION:
APPLICATION UNMER: US 60/045,725
FILING DATE: 06-MAY-1998
CLASSIFICATION UNMER: 33,878
REFERENCE/DOCKET NUMBER: 4-97
TREECOMMUNICATION INFORMATION:
TRELEPHONE: (303) 499-8080
TRELEPACE (100CKET NUMBER: 4-97
TREECOMMUNICATION INFORMATION:
TELEPACE (1303) 499-8089
INFORMATION FOR ESC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 749 base pairs
TYPE: DNA (99-8089)
INFORMATION FOR ESC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 749 base pairs
TYPE: DNA (99-8099)
INFORMATION FOR ESC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 749 base pairs
TYPE: DNA (99-8099)
INFORMATION FOR ESC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 749 base pairs
TYPE: DNA (99-8099)
INFORMATION FOR ESC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 749:
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Maximum Match 100%
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Maximum DB
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    987654321
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length: 2000000000
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1: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA199.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1991.DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT:*
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  2815
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                                                       AAZ88725
AAT34162
ABL11013
ABL09420
ABL11012
ABL34419
                    ABL18046
AAT80200
ABL10307
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                                                                                              Human CD95 recepto Fas promoter regio Drosophila melanog Drosophila melanog
                                                                                                                                                                                              Description
                  Human immune syste
Drosophila melanog
Phosphatidyl inosi
  Drosophila
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  melanog
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## ALIGNMENTS

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RESULT
AAZ88725
Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy \,
                                                                                                                                                                                                  p53; CD95 receptor; human; screening; apoptosis-modulation; cancer chemotherapy; ss.
                                                                                                                                                                                                                               Human CD95 receptor promoter DNA p53 binding fragment #3.
                                                                                                                                                                                                                                                                                          AAZ88725 standard; DNA; 20 BP.
                                                         Krammer P, Mueller-Schilling M, Oren
                                                                                                                   16-OCT-1998;
                                                                                                                                       03-FEB-2000.
                                                                                                                                                            DE19847779-C1.
                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                   11-MAY-2000
                                                                                                                                                                                                                                                                         AAZ88725;
                                                                            (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                 16-OCT-1998;
                                      2000-162245/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor promoter which is capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 8 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene promoter; apoptosis; ageing; autoimmune disease;
ell senescence; ss.
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             /function= CP2 t
/note= "claim 6"
1075..1476
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/note= "claim 5"
1037..1043
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                                                                                                                                                                                                                                                                                              /function= GF-1 transcription /note= "claim 7"
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                                                                                  /*tag=
                                                                                                                                                                                                                                  'function- NF-Y
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/note= "claim 9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'function= GF1 transcription factor binding site note= "Claim 7"
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/note= "Fas
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Best Local
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                          27-SEP-2001.
23-MAR-2001; 2001WO-US09231.
                                                    WO200171042-A2
                                                                         Drosophila melanogaster.
                                                                                                     pharmaceutical;
                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ ID NO 27521.
                                                                                                                  Drosophila;
                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                               ABL11013;
                                                                                                                                                                                                                     ABL11013 standard;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1608 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                           malignancies and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A novel DNA segment (AAT34162) has an isolated sequence region defined as the Fas gene promoter region. This includes a number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 2; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Fas gene promoter region - used : expression and for developing products apoptosis disorders
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                                                                                                            developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                   (first entry)
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                                                                                                    gene;
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/product= Fas protein leader
1497..1608
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                                                                                                                                                                                                                                                                                                                                                                                                  398 A; 421 C; 423 G; 366 T; 0 other;
                                                                                                                                                                                                                     cDNA; 1737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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11-JUL-2000;
New isolated nucleic
                      WPI; 2001-656860/75
P-PSDB; ABB65317.
                                                                                                      23-MAR-2000;
11-JUL-2000;
                                                                                                                                       23-MAR-2001; 2001WO-US09231
                                                                                                                                                               27-SEP-2001
                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                          Drosophila melanogaster
                                                                                                                                                                                                                                  pharmaceutical; gene; ss.
                                                                                                                                                                                                                                            Drosophila; developmental biology;
                                                                                                                                                                                                                                                                   Drosophila melanogaster expressed polynucleotide
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                                                        Venter JC,
                                                                               (PEKE ) PE CORP NY.
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2000US-0614150
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2000US-0614150.
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 detection reagent for detecting 1000
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Pred. No. 13;
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                                                                                                                                                                                                                                             signalling; insecticide;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                           Claim 1; SEQ ID NO 27518; 21pp + Sequence Listing; English.
                                                                                                                                                                                             genes from Drosophila
                                                                                                                                                                                                                 New isolated nucleic
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
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2000US-0614150
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94.7%;
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                                                                                                                                                                   The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                           Sequence 1608
                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                            cytosine methylation
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01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPIGENOMICS AG.
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                                                                                                                                                   The present sequence is a gene of the
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                     Length 1608;
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AAT80200
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                      AAT80200 standard;
                                                                                                                                                                                                        Sequence 2279 BP;
                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                            The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 5611; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                         Conservative
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cal; gene; ds.
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                      cDNA; 6831 BP
                                                                                                                                                    84.0%;
90.0%;
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                                                                                                                                                                                                                                        this patent did not form part of the printed obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                  detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
                                                                                                                                       0,
                                                                                                                                                                Score 16.8;
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22-JUN-1998

(first entry)

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ABL10307
ID ABL1
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AC ABL1
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                                                                                                                                                                                                               This cDNA sequence codes for cpk (see AAW38757), a Drosophila copolypeptide that belongs to a novel class of phosphatidyl inositol 3 kinases that contain a C2 domain, are capable of phosphorylating a D3 hydroxyl of an inositol ring in phosphatidyl inositol and copoline of phosphorylating a D3 hydroxyl of an inositol ring in phosphatidyl inositol and copoline control e.g. cell cycle progression and intracellular protein control e.g. cell cycle progression and intracellular protein corting. Short fragments of cpk cDNA were obtained from a D7 copophila cDNA library by PCR (see AAM50195-96). These short compared to screen the cDNA library to obtain larger fragments were used to screen the CDNA library to obtain larger fragments, and missing 5 ends were obtained by RACE. A recombinant host cell, transfected with a vector comprising a cpk can be used to screen for agonists/antagonists of activity and concerned method of treating a disorder caused by dysregulation cof a growth factor activation signalling cascade. Antagonists cof activity and concerned comprise such as atherosclerosis, inflammatory joint disease, cc psoriasis, restenosis following angioplasty, and cancer.
                                                                                                                                                           Query Match
                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated phospatidyl inositol-3 kinase polypeptide - used to develop products for diagnosis and therapy, particularly for proliferative disorders, e.g. inflammatory joint diseases, or cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-FEB-1996;
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          ABL10307;
                                   ABL10307 standard;
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                                                                                                                                                                                                Sequence 6831 BP; 1829 A; 1685 C; 1669 G; 1648 T; 0 other;
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                                                                                                                                                  Local Similarity
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                                   CDNA; 6871 BP
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 25403; 21pp + Sequence Listing; English.
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                                            pharmaceutical; gene;
                                                               Drosophila; developmental biology; cell signalling;
                                                                                                              Drosophila melanogaster genomic polynucleotide SEQ ID NO 11830.
                                                                                                                                                               26-MAR-2002
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Drosophila melanogaster
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Pred. No. 31;
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Best Local
                New isolated nucleic
                                                                   WPI; 2001-656860/75.
                                                                                                                      Venter JC,
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanogaster.
                                                                                                                      Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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90.0%;
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                                                                                                                 PWD,
             detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Pred. No. 3;
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                                                                                                                   Myers
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        detecting 1000 or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insecticide;
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capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511) and the encoded proteins
                                                                                  The invention relates to an isolated nucleic acid detection reagent
                                                                                                                      Claim 1;
                                                                                                                                                                              New isolated nucleic
                                                                                                                                                                                                             P-PSDB; ABB66203
                                                                                                                                                                                                                                                         Venter JC,
                                                                                                                                                                                                                                                                                    (PEKE ) PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster expressed polynucleotide SEQ ID NO 25400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL10306 standard; cDNA; 17358 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA commissions and pharmaceutical drugs.
                                                                                                                                                     interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 11827; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes from Drosophila and for elucidating cell signalling and
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                                                                                                                                                                                                                           2001-656860/75
                                                                                                                                                              solated nucleic acid from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                  SEQ ID NO 25400; 21pp + Sequence Listing; English
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Pred. No. 34
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The invention relates to isolated breast tumour proteins and conclude acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the corrections. Also included are expression vectors expressing the proteins and substitute the proteins or concluded an antipolate in the protein protein and treatment of concleic acids may be used in the prevention, diagnosis and treatment of concleic acids may be used in the prevention, diagnosis and treatment of concleic acids and their complements may also be used as DNA probes in diagnostic catals and their complements may also be used as DNA probes in diagnostic casasys to detect and quantitrate the presence of similar nucleic acids in concleic, and therefore which patients may be in need of restorative concleins, nucleic acids and antibodies may be used in assays to detect and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the proteins in casmiles (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other complements for detecting the presence of the proteins in the construction of the proteins in the presence of the proteins in the construction of the proteins in the construction of the proteins in the construction of the
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08-JUN-2000; 2000US-0590751.
22-JUN-2000; 2000US-0604287.
20-JUL-2000; 2000US-0620405
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 165; 297pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast cancer protein; tumour; cancer;
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Pred. No. 34;
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23-JUN-1999;
02-SEP-1999;
03-NOV-1999;
                                                                                                          The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers,
                                                                                                                                                                a breast tumor protein
                                                                                Sequence 1022
                                                                                                  particularly breast tumours.
                                                                                                                                                Claim 6; Page 105-106;
                                                                                                                                                                          An isolated polypeptide useful for the treatment and diagnosis of tumors e.g. breast cancer comprises at least an immunogenic porti-
                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                       Yuqiu J,
                                                                                                                                                                                                                                                                                                         15-FEB-2000; 2000WO-US05308
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                                                                                                                                                                                                                                                                                                                                             WO200060076-A2
                                                                                                                                                                                                                                                                                                                                                               Ното
                                                                                                                                                                                                                                                                                                                                                                                 Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                   Human breast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1022 BP; 254 A;
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99US-0389681.
99US-0433826.
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                                             Score 15.8;
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23-JUL-1998 (first entry)

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Search completed: September 7, 2002, 18:40:29 Job time: 29923 sec
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                              This sequence encodes a novel human type II gonadotropin-releasing hormone receptor (GnRHR II) polypeptide. This protein and its products can be used for identifying compounds which modulate GnRHR II-mediated metabolism in cells. Compounds identified as agonists or antagonists can be used for treating hormone-dependent tumours. Agonists and antagonists may also prove useful in the study of GnRHR II-directed neuromodulation of sexual behaviour, e.g. agonists may be used in the treatment of diminished libido and impotence. The products can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated type II gonadotropin-releasing hormone receptor - used to develop products for use in the treatment of hormone-dependent tumours or for neuromodulation of sexual behaviour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Type II Gonadotropin releasing hormone receptor; GnRH-H II; impotence; identification; diagnosis; detection; modulator; treatment; libido; hormone-dependent tumour; neuromodulation; sexual behaviour; ds.
                                                                                                                                                                                                                      Sequence 1642 BP; 449 A; 399 C; 324 G; 470 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 37-38; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-168750/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conklin DC,
Troskie B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCA-) UNIV CAPE TOWN. (ZYMO) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-1996;
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                                                                             788 acctacctaatagctatct 806
                                                                                            2 aactacctaagagctatct 20
                                                                                                                                                                                                                                                       detection and diagnosis
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Sequence Sequence

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                Score
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                Description
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1 (bases 1 to 20)

Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 16 03-FEB-2000;

DEUTSCHES KREBSFORSCH (DE)
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Sequence 16 from Patent
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/db_xref="taxon:9606"
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D31968 Human DNA f
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AC025616

Homo sapi

PAT 16-SEP-2000

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Mueller-Schilling,M., Krammer,P. and Oren,M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy patent: DE 19847779-C 30 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE)
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Mueller-Schilling, M., Krammer, P. and Oren, M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 22 03-FEB-2000;

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/db_xref="taxon:9606"
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Krammer, P.H.
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Behrmann, I., Walczak, H. and Krammer, P.H. Structure of the human APO-1 gene
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1877)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-OCT-1994) J. Cheng, Univ.of Alabama at Birmingham, Univ. of Alabama, 701 South 19th Street, UAB Station, LHRB 473, Birmingham, AL 35,294-0007, USA Related sequences: M67454 and X63717.
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Cheng, J., Liu, C., Koopman, W.J.
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Immunol. 24 (12), 3057-3062 (1994)
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1075. .1496
/gene="Fas, Apo-1"
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/db_xref="taxon:9606"
/tissue_type="placenta"
/clone_lib="placental genomic DNA"
/map="10q23 or 10q24.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heidelberg,
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/product="APO-1"
1689. .1810
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/gene="APT"
/label=ex1b
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join(1653. .1810, x81336.1:155. ...
x81338.1:145. .253, x81339.1:552.
x81341.1:255. .279, x81342.1:103.
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/oin(1670. 1810, x81336.1:155. .320, x81337.1:146. .283,

/x81338.1:145. .253, x81339.1:552. !613, x81339.1:766. .82

/x81340.1:79. .161, x81341.1:255. .279, x81342.1:103. .175
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1653. .1810
                                                                                                                                                                                                                                                                                   /label=HsmRNA4
/product="APO-1"
1704. .1810
                                                                                                                                                                                                                                                                                                                                                     join(1704. .1810, x81336.1:155. .320, x81337.1:146. .283, x81338.1:145. .253, x81339.1:552. .613, x81339.1:766. .828, x81340.1:79. .161, x81341.1:255. .279, x81342.1:103. .1757)
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1670. .1810
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/clone="cAPO-1"
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join(1707. .1810,x81336.1:155. .320,x81337.1:146. .2
x81338.1:145. .253,x81339.1:552. l.613,x81339.1:766. .2
x81340.1:79. .161,x81341.1:255. .279,x81342.1:103. .
/gene="APT"
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/chromosome="10"
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/product="APO-1"
1708. .1810
                                                                                                                                                                                                            /usedin=X81335:HsmRNA4
                                                                                                                                                                                                                                                   /label=ex1d
                                                                                                                                                                                                                                                                      /qene="APT"
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                                                                                                                                           /number=
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2. !828, x81340.1:79. .161,
3. !1757)
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.>1757)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:nakanaka@dbs.p.kanazawa-u.ac.jp, Tel:076-234-4424, Fax:076-234-4480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection J. Biol. Chem. 270 (30), 18007-18012 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wada, N., Matsumura, M., Ohba, Y., Kobayashi, N., Takizawa, T. Nakanishi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2165)
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llarity 100.0%;
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join(1708. 1810,X81336.1:155. .320,X81337.1:146. .283,

X81338.1:145. .253,X81339.1:552. .613,X81339.1:766. .828,

X81340.1:79. .161,X81341.1:255. .279,X81342.1:103. .>1757)

/gene="APT"
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276. .284
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/db_xref="taxon:9606"
/clone="pF7"
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/label=ex1f
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                                                                      1436. .1781
                                                                                                                                                                                                                                                                                                                                       /tissue_type="blood"
                                       /number=
                                                                                         /bound_moiety="NF-IL6"
                                                                                                                          /bound_moiety="Ets"
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   /codon_start=1
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                             سا
              aaactacctaagagctatct 20
AAACTACCTAAGAGCTATCT 1403
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-MAY-1995) F.H. Rudert, Genesis Research & Development, Corporation Ltd., PO Box 50, Auckland, NEW Overlaps with X81335, & x82279-x82286.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rudert, F.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96069539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Cell Biol. 14 (11),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watson,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rudert, F., Visser, E., Forbes, L., Lindridge, E., Wang, Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2344)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identification of a silencer, enhancer, and basal promoter region
in the human CD95 (Fas/APO-1) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta interferon; CD95 gene; silencer.
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                                                          Conservative
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                                                                                                                                        /note="basal promoter"
546 c 511 g
                                                                                                                                                                         /note="lysozyme silencer 1"
1338. 1919
1920. .2344
                                                                                                                                                                                                              /note="beta interferon silencer
complement(1237. .1244)
                                                                                                                                                                                                                                               /note="silencer"
717. .801
                                                                                                                                                                                                                                                                                        /tissue_type="placenta"
/map="q24.1"
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                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                      /germline
                                                                                                                                                                                                                                                                                                                                  'chromosome="10"
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/protein_id="BAA20850.1"
/db_xref="GI:4433150"
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Pred. No.
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Sequence
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1 (bases 1 to 2827)

Mueller-Schilling, M., Krammer, P. and Oren, M.

Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy

Patent: DE 1984779-C 4 03-FEB-2000;

DEUTSCHES KREBSFORSCH (DE)

Location/Qualifiers
                          AX026089
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Sequence 4 from Patent DE19847779.
AX026092
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Nuceller-Schilling,M., Krammer,P. and Oren,M.
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Sequence 3 from Patent DE19847779.
AX026091
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                                                                                                                                                                                                                                                            corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX026089.1 GI:10187520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on Aug 31, 2001 this sequence version replaced gi:14161146. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human DNA sequence from clone RP11-399019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 3212)
Mueller-Schilling, M., Krammer, P. and Oren, M.
                    http://www.sanger.ac.uk/HGP/Chr10
RP11-399019 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10 constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blakey, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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http://www.chori.org/bacpac/home.htm
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COPIE, A.D. CHOWALLY, I., CHILLSCOPPOLICS, C., LEVELAND, C.D.
COYLE, M.D., Dathorne, S.R., David, R., David, R., Davis, C.,
COYLE, M.D., Dathorne, S.R., David, R., David, R., Delgado, O.,
Davy-Carroll, L., Decerich, D.A., Delaney, K.R., Delgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
FOSTER, P., Gall, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M.,
Morgan, M., Morris, S., Moser, M., Nickerson, J., Nwokenkwo, S.,
Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J. Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burce,S., Burcell,K.L., Byrd,N.C., Carron,T.F., Carracos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Carracos,S.R., Chacko,J., Chavez,D., Chen,G., Cox,C., Chen,Z., Chowdhry,I., Christoppulos,C., Cleveland,C.D., Cox,C., Chen,Z., Chowdhry,I., Christoppulos,C., Cleveland,C.D., Cox,C.,
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/note="Sequence confirmed by AC015461 sequenced by WIBR."
<sub>1</sub> 36398 c 36888 g 58358 t
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            findPhrapList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 172269)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                               runs of N, b
                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 145908 bases at least Q40 Consensus quality: 152564 bases at least Q30 Consensus quality: 158487 bases at least Q30 Estimated insert size: 150457; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.7x in Q20 bases; sum-of-contigs estimation
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                                                                                                              Submitted (20-AUG-2001) Whitehead Instituté/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                     Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus, clone RP23-57F18
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                             Direct Submission
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/clone="Ct230-205114"
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167425: gap of unknown length
168496: contig of 1071 bp in length
168596: gap of unknown length
169938: contig of 1342 bp in length
170038: gap of unknown length
171167: contig of 1129 bp in length
171267: gap of unknown length
172269: contig of 1002 bp in length
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Institute/ MIT Center
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for Genome Research
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                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9344: contig of 9344 bp in length
9345 9444: gap of
9445 13083: contig of 3639 bp in length
13084 13183: gap of
13184 15745: contig of 2562 bp in length
15746 15845: gap of
15846 20539: contig of 4694 bp in length
20540 20639: gap of
20640 62896: contig of 42257 bp in length
20640 62896: contig of 42257 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 250000; agarose-fp
Insert size: 245397; sum-of-contigs
Quality coverage: 9.9 in Q20 bases; agarose-fp
Quality coverage: 10.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 242847 bases at least Q40
Consensus quality: 244315 bases at least Q30
Consensus quality; 244906 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project Information Center project name: L14296 Center clone name: 57_F 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193685 193784: gap of 100 bp
193785 245997: contig of 52213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                              62997. .193684
/note="assembly_fragment"
193785. .245997
                                                                                                                                                                                                                                         vector_side:right"
                                                                                                                                                                                                                                                                clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="RP23-57F18"
                                                                                                                                                                                                                                                                                  note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
20640. .62896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                        49514 c
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193684: contig of 130688 bp in length
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Pred. No.
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7.1;
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web Site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guardin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cdna@fruitfly.berkeley.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1814)
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                                                                                                             /codon_start=1
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/SIAALMYYQRUKIKERSEKALKKORKKYKEOEDEKTTPVPEDPPYYEAGTEVEDGLR
ILEALAATGLRSIRYAQEIAGVRQIVANDLSRQAVASINTNIRHNKVEELIEPSHSDA
MTLMYLSTQPEKRFDAVDLDPYGCPNRFLDGANQCLVDGGLLLVTAATDMAVLAGNAPE
ACYVKYGSVPLRMKCCHEMALRILLHCIESHANWYGKYIEPLLSISADFYIRIFVRVY
VGQAQCKLSMKSKOSWIYQCTGCETFTLQPLGITKPNPTAGNPQQLKFGIPTGGAVNSQ
CEHCGHRHHLGGPIWSAPIHNPETYQDLLTAYQETTLQSLGTORRITYGVLSNVQEELQ
DVPLYYTPDKLCCVLKLEIVPMLKFRSAILHAGYRVSYSHASKNSLKTNAPPAVLWDI
DVPLYYTPDKLCCVLKLEIVPMLKFRSAILHAGYRVSYSHASKNSLKTNAPPAVLWDI
DVPLXYTPDKLCCVLKLEIVPMLKFRSAILHAGYRVSYSHASKNSLKTNAPPAVLWDI
                                                                 TPHWGPGTRATIMIGDNKLPKSYRNQNKKQRHKASEQQAEDDQQDTPQAVDEYDGDVE
                                                                                                         LRSWSKRHPVNPERMIPGSPLAAILSKECTAVYEFDELHPEANPKSRKSALSRFQENP
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="33D5-33E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Longest ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="CG6388"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="alignment with genomic scaffold AE003636"
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Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C. M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Moshrefi, B., Poon, L., Sequeira, A., Sethi, H., Shir, E., Land, C., Land
                                                                                                                                                                                                                                                                                                                                                                   This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Sep 6, 2001 this sequence version replaced gi:13324753
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (06-AUG-1999) Drosophila Genome Center, Laboratory, MS 64-121, Berkeley, CA 94720, USA On Sep 6, 2001 this sequence version replaced gi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rubin, G.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                      /db_xref="taxon:7227"
/chromosome="2L"
                                                                                                                                                                                 /strain="y; cn bw sp"
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
/clone="BACR05E09 (D865)"
                                                                                                                                                                                                                            organism="Drosophila melanogaster"
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/clone\_lib="RPCI-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI in pBACe3.6)"

BASE COUNT 47347 a 29741 c 30511 g 47172 t

Query Match 87.0%; Score 17.4; DB 3; Length 154771; Best Local Similarity 94.7%; Pred. No. 53; Matches 18; Conservative 0; Mismatches 1; Indels 0;

Indels 0; Gaps

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Search completed: September 7, 2002, 18:23:58 Job time: 28937 sec

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Maximum Match 100%
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Maximum DB
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  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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length: 2000000000
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Copyright (c) 1993 - 2000 Comp
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US-09-290-640-1
US-08-444-231-18
US-08-152-443A-18
US-08-219-237B-1
US-08-219-237B-1
US-08-232-463-14
US-08-232-463-14
US-08-232-463-14
US-08-232-463-19
PCT-US93-06-251-19
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US-09-018-594A-3
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Sequence 19, Appl Sequence 13, Appl	Sequence 26, Appl Sequence 10, Appl	Sequence 8, Appli Sequence 11, Appl	Sequence 3, Appli Sequence 3, Appli	10,	Sequence 11, Appl	Sequence 11, Appl	Sequence 27, Appl	Sequence 2, Appli	Sequence 24, Appl				

## ALIGNMENTS

US-09-290-640-1

; Sequence 1, Application US/09290640 ; Patent No. 6204055

GENERAL INFORMATION:

APPLICANT: Dean, Nicholas M. APPLICANT: Marcusson, Eric G. TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling FILE REFERENCE: ISPH-0351

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; ISSUE: 15
; PACES: 10709-10715
; DATE: 1992-05-25
; DATABASE ACCESSION NUMBER: X63717/Genbank
; DATABASE ENTRY DATE: 1996-07-19
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LOCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 267
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                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                Query Match
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CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 25
TYPE: DNA
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                               2187
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                                                                                                                                                                                                     2007 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 2066
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                                                         ttggggaagetettteaetteggaggattgeteaacaaceatgetgggeatetggaceet
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Best Local Similarity
Matches 226; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
2153 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg
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REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
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APPLICANT:
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APPLICATION NUMBER: US,
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/152,443 FILING DATE: 15-NOV-1993
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STATE: Californi
                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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SHAPIRO, JOHN P.
KIEFER, MICHAEL C.
KIEFER, MICHAEL C.
NOVEL FAS PROTEIN AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415) 494-0792
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                                                                                                                                                                                    Score 226; DB 1;
Pred. No. 9.9e-53;
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Best Local Similarity
                                                                                                                                                                                     Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                     2033
               2153 ctcccgcgggttggtggacccgctcagtacggagttggggaagctctttcacttcggagg 2212
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NAME/KEY:
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TELECOMMUNICATION INFORMATION: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KLEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAX
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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   121
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                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 15-NOV CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 755 ray.
CITY: Palo Alto
                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                          ggcactggcacggaacacaccctgaggccagccctggctgcccaggcggagctgcctctt 2152
                                                                                                                                      gacgcttctggggagtgagggaagcggtttacgagtgacttggctggagcctcaggggcg 2092
                                                                                                                     GACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCC
                                                                                                                                                                                 226;
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Pred. No. 9.9e-53;
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APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Sufface Antigen
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/872,129
FILING DATE: 22-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                      NAME/KEY: mat_peptide LOCATION: 243..1199 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 195..1202
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 28-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                    NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                            NAME/KEY: sig_peptide LOCATION: 195..242
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                                   IDENTIFICATION METHOD:
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T: P.O. Box 2266 Eads Station
Arlington
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Best Local 9
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                                                                                          TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAGATA, Shi
APPLICANT: ITOH, NAOTO
APPLICANT: YONEHARA, SI
                                                                                                                        REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                              APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                            TELEPHONE: 703-205-8050
                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
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                              STRANDEDNESS:
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                   TOPOLOGY:
                                            TYPE: nucleic acid
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cDNA to mRNA
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                                                                                                                                                                  28,977
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                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 16
LENGTH: 2534
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/09180100 Patent No. 6306395
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Best Local Similarity 100.0%;
Matches 226; Conservative
                                                                     Matches 226;
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/180,100 CURRENT FILING DATE: 1998-11-02 EARLIER APPLICATION NUMBER: PCT/JP97/01502 EARLIER FILING DATE: 1997-05-01
                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
                                                                                                                                                                         TYPE: DNA
2213 attgctcaacaaccatgctgggcatctggaccctcctacctctggt 2258
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LOCATION:
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100.0%; Pr
                                                              Score 226; DB 4; Length 2534; Pred. No. 1e-52; 0; Mismatches 0; Indels
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Best Local :
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Patent No. 5670367
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                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECO
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ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
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454 tttggctacatttttttatttgtaaagtaagtttaataatcactcatctcactgggctat 513
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                                                                                                        Local Similarity
nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                   2.5%; Score 79.4; DB 1; ilarity 5.4%; Pred. No. 1.3e-11; Conservative 224; Mismatches 125;
                                                                                                                                                                                                                                          linear
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                                                                                                                                      Length 7218;
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                                                                                                                                                 APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMTELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                         SEQUENCE CHARACTERISTICS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                            FILING DATE
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                                            STRANDEDNESS:
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1800 Diagonal Road, Suite 500
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                                                                                                                                      (703)683-4109
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Patent No. 5734039
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ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                             SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                             APPLICATION NUMBER: | FILING DATE: Septemb CLASSIFICATION: 514 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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OPERATING SYSTEM:
                                                                                                  FILING DATE:
                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                           CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                              Pennsylvania
                                                                                                                                                                                                                                                                                                                                                        Two Penn Center, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 67.8; DB 1; ilarity 8.2%; Pred. No. 2.1e-08; Conservative 227; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calabretta, Bruno
                                                                                                                                                                                                                                            IBM PS/2
                                                                                                                                    : US/08/306,691B
: September 15, 1994
: ON: 514
                                                                                                                                                                                                                                                            Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                                                                                                                                                      ANTISENSE
OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
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TELEFAX:

(215) 568-5549

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PCT-US93-06251-19
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PCT-US93-06251-19
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 115;
                                                                                                       TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                             NAME: DIGIGIIO, Frank S. A6
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-433
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO:
                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Trivalent Synthesis of Carly Invention: Stereospecific Alkylphosphonates and Arylphosphonates NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
           TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wickstrom, Eric and Rife, Jason P. TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3986 TTCTTTCTTTTTCTATCTTTTGAGA 4012
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LENGTH: 35100 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                            STRANDEDNESS:
                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Garden City
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TOPOLOGY: 11
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Pred. No. 1e-05;
0; Mismatches 92;
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PCT-US95-17083-7
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GENERAL INFORMATION:
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Best Local Similarity
Matches 115; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 857 base pairs
TYPE: nucleic acid
                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                       NUMBER OF SEQUENCES: 16 CURRENT APPLICATION DATA:
                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 1
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APPLICATION NUMBER: PC'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534 gaagatccacatatgtgagttgctggcttataattcacactcaagagatactgattttgt 593
                                                                                                               FILING DATE: CONTROL CLASSIFICATION:
STRANDEDNESS:
                TYPE:
                                                                      FILING DATE:
                                                                                   APPLICATION NUMBER:
                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGTTGCAGTGAGCTGAGATCATGCCACTGCACTCCAGCCTAGGCGACAGAGCAAGACT 3865
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                        920 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                      23-DEC-1994
FO TD NO: 7:
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                                                                                                                                                                                    SECRETED HUMAN FAS ANTIGEN
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                                                                                   USSN 08/371,263
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SEQUENCE CHARACTERISTICS:
LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application PC/TUS9517083 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.8%; Score 57; DB 5; La Best Local Similarity 100.0%; Pred. No. 5.8e-06; Matches 57; Conservative 0; Mismatches 0;
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                                          Matches
                                                                         Query Match
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                                                                                                                                                                                                           APPLICATION NUMBER: USSN
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2202 cacttcggaggattgctcaacaaccatgctgggcatctggaccctcctacctctggt 2258
                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SECR NUMBER OF SEQUENCES: 16 CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 23-DEC-
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CURRENT APPLICATION DATA:
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                                                                                                                                                                      TYPE: nucleic acid
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1.8%; Score 57; DB 5; L
Local Similarity 100.0%; Pred. No. 5.6e-06;
hes 57; Conservative 0; Mismatches 0;
                                         Local Similarity
nes 57; Conserv
                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US95/17083 FILING DATE: CONCURRENTLY HEREWITH
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                                                                                                                                              TOPOLOGY:
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                                   1.8%; Score 57; DB 5; Locality 100.0%; Pred. No. 6.3e-06; Conservative 0; Mismatches 0;
                                                                                                                                           linear
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                                                                     Length 1104;
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Search completed: September 7, Job time: 28759 sec
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                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 0
FILING DATE: 23-DEC-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                    Query Match 1.8%; Score 57; DB 5; Le Best Local Similarity 100.0%; Pred. No. 6.5e-06; Matches 57; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application PC/TUS9517083 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17083
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                       1 CACTTCGGAGGATTGCTCAACAACCATGCTGGGCATCTGGACCCTCCTACCTCTGGT 57
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                   2002, 18:21:05
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Listing first 45 summaries
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             Pending_Patents_NA_Main:*

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13: /cgn2_6/ptodata/2/pna/USO9_COMB.seq:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.

Score

Query Match Length DB

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Sequence 14682, A Sequence 14682, A Sequence 11167, A		1584	Sequence 21, Appl Sequence 327, App	2456	5939	Sequence 3031, Ap	2083	4919,		4924,	10283,		Sequence 9888, Ap	674,	Sequence 674, App	Sequence 2, Appli	Sequence 29531, A	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	w	9	94	Sequence 4, Appli	Sequence 10, Appl	Sequence 1, Appli

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CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILLING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martin
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Area
FILE REFERENCE: 4121-122
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US-09-834-291-1
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Best Local Similarity
Matches 3212; Conserv
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TYPE: DNA
ORGANISM: HOMO
5-09-834-291-1
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US-09-652-911-8889

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                                                                                                       SEQ ID NO 10
LENGTH: 45121
                                                                                                                                PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                              APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
CURRENT FILING DATE: 2001-11-37
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Best Local
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
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SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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APPLICANT: Wyatt, Jacqueline
TITLE OF INVENTION: Antisense Modulation of
FILE REFERENCE: ISPH-0502
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NUMBER OF SEQ ID NOS: 179
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RESULT 5
US-09-802-669-94
US-09-802-669-94
Sequence 94, Application US/09802669
GENERAL INFORMATION:
APPLICANT: MARCUSSON, Eric G.
APPLICANT: MARCUSSON, Eric G.
APPLICANT: MYATT, Jacqueline
APPLICANT: MYATT, Jacqueline
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT APPLICATION NUMBER: US/09/802,669
PRIOR APPLICATION NUMBER: US/09/865,615
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
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Matches 2158; Conserv
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LENGTH: 2165
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; LENGTH: 2380
; TYPE: DNA
; ORGANISM: HOMO 9
US-09-834-291-3
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/0343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
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Best Local Similarity
Matches 2348; Conserv
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FILE REFERENCE: 4121-122
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Muller-Schilling, Martina
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9006	gtctctgatctcg	194
1946 1500	7 cgcgcgcaggccaagttgctgaatcaatggagccctccccaacccgggcgttccccagcg 1 	188 <sup>*</sup> 144 <sup>*</sup>
1886 1440	7 tgcccatttgtgcaacgaaccctgacttccttcctcaccctgacttctcccccttcctt	182
1826 1380	7 ctcgaggtcctcacctgaagtgagcatgccagccactgcaggaacgccccgggacaggaa 1 	176 <sup>-</sup> 132
1766 1320	7 ctccccaacttcccaggttgaactacagcagaagcctttagaaagggcaggaggccggct :	
1706 1260	7 gccaaggctcctgtacccaggcaggacctctgcgctctgagctccattctccttcaagac:	164 120
1646 1200	7 caacatggacagcccagtcaaatgccccgcaagtctttctctgagtgactccagcaatta 	158 114
1586 1140	7 tttttcatatggttaactgtccattccagaaacgtctgtgagcctctcatgttgcagcca	152 108
1526 1080	7 ttgagaaataaaaactaaggggccctcccttttcagagcccttatggcgcaacatctgtac	N 6
1466 1020	7 gaatgtttaatatagctggggctatgcgatttggcttaagttgttagctttgttttcctc 	6 0
1406 960	7 tttttttttaaagaaaattggccaggaaataatgagtaacgaaggacaggaagtaattgt 	134 90
1346 900	7 ccgttccaaagcaatagtgactttgaacagtgttcaccagagcacgaaagaattacaaga 	4 4
1286 840	7 atgtcattatocaaacatacottotgtaaaattoatgotaaactacotaagagotatota 	
1226 780	7 aatactgaaacctttagtgtgtccagtctggaactgcatccaaattcaggttcagtaatg	116 72
1166 720	07 aattgggaagggagagaggttgcagagtgaggttgcagagcttggtggacgatgccaaagg 	110
1106 660	47 tgaaggatgaacagtgggctaagcaaagggttattaatgtgtttattaatgggttgaatct 	104
1046	88 ctaacctagatttgagggccc-aacaggctccagaagaaaatgtcaactgagaggaagcc 	98 54
987 540	28 gtggtaagtgcagtgacagatgcaaaacacagggtgatggaaagccctcaggagggtaac 	92 48
927 480	68 ggcactaacagtctactgaaaggtggaacagagacaagcctatcaacacctacaagactg 	86 42

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3026	ttttgtttttctgcccttct	2967	Qy
2966 2127	accytttttattytcacacagaaaaggaaactgccttytctcccttccgggaattctct;	2068	Qy Db
2906 2067		0 0	Db VY
00	agacgtaggaaataagtcagcaccgaagcagtggttaagccggagggctcggaagaacg 	94	Db Vy
2786 19 <b>47</b>	yyyyyyyyyagagagoctgoagocttcagaacacatattgctcattttctggcagttct 	88	Db X
2726 1887	<pre>ictgacaagccaagccaaaggtccgctccggcgcgggtgggt</pre>	8 6	Db Qy
2666 1827	ctttagggtcgctggaggggaccccggttggagagaggagcggaactcctggacaagc 	76	Db Qy
2606 1767	tgcgctccacgttgaggtgggcgtggggggggggacaggaattgaagcggaagtctgggaa    aa	7 5	ф
1765		76	Db
2546	gatgcgaagtgctgatcccgctgggcaggcggggcagctcccggcgctcctcggagaccac	4	Qy
1765		1766	Db
2486	aggaccttccctcaggcccgggtgctcagaacgatggaggacttgcttttcttgggcctt	2427	Qy
1765		1766	Db
2426	ggcacctgggagcggcgggctgctgcgggaggcgttggagactggctccccggggggctgtt	2367	Qy
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1740		1741	Дb
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2066 1620	7 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 	2007 1561	Qy da
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Best Local Similarity
                                                                                   Matches
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                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Sertich, Gary J.
REGISTRATION UNMBER: 34,430
REFERENCE/DOCKET NUMBER: UOAB
TELECOMMUNICATION INFORMATION:
TELEPHAN: 512/414-3000
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: 1
APPLICANT: 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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LENGTH: 1608 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                FEATURE:
                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Arno
STREET: P.O. BC
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
            827
                                                            767
                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 20-JAN
                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                        TOPOLOGY:
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gagtgtgtgcacaaggctggcacgcccagggtcttcctcatggcactaacagtctactga
                                                                                   1582;
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N: 435
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Pred. No. 0;
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             gtgagcatgccagccactgcaggaacgccccgggacaggaatgcccatttgtgcaacgaa
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  CCCTGACTCCTTCACCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGC
                                                           AAATGCCCCGCAAGTCTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCA
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                                                                                                                                          TELEFAX: (713) 777-6908
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
                                                      TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         TELEPHONE: (713) 777-2321
            HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: U
FILING DATE: January
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Huma
FRAGMENT TYPE
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adl
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STATE: TX
ZIP: 77071
                                                                                                                                                                                                     NAME: Benjamin Aaron Adler, Ph.D., REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919
                                      DESCRIPTION:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                 LENGTH:
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IMMEDIATE SOURCE:
LIBRARY: (FIXII; EMBL-SP6/T7
CLONE: FIXI, FIX2, FIX3; EMBL1, EMBL2, EMBL3
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aaatgccccgcaagtctttctctgagtgactccagcaattagccaaggctcctgtaccca
                                                             tocattocagaaacgtotgtgagcototoatgttgcagcoacaacatggacagcocagtc 1605
                                                                                                        ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg 1185
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                     TCCATTCCAGGAACGTCTGTGAGCCTCTCATGTTGCAGCCACAAGATGGACAGCCCAGTC
                                                                                                                                                                                               CCTTCTGTAAAATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTG
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Pred. No. 0;
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US-08-377-522D-1; Sequence 1, Application US/08377522D; GENERAL INFORMATION:
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        COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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ZIP: 7
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APPLICATION NUMBER:
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US/08/377,522D
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                                                                                                                                                                              1066
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ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: D5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: (FIXII; EMBL-SP6/T7 CLONE: FIX1, FIX2, FIX3; EMB POSITION IN GENOME:
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STRANDEDNESS: double-stranded
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                                                                                                                                           ttgcagagtgaggtgcagagcttggtggacgatgccaaaggaatactgaaacctttagtg
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ccttctgtaaaattcatgctaaactacctaagagctatctaccgttccaaagcaatagtg
                                                                  TGTCCAGTCTGGAACTGCAACTCCAAATTCAGGTTCAGTAATGATGTCATTATCCAAACATA
                                                                                 tytccagtctggaactgcatccaaattcaggttcagtaatgatgtcattatccaaacata
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Pred. No. 0;
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Best Local
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US-60-324-185-29531 RESULT 10 APPLICANT: Mortis, MacDonald
APPLICANT: Lal, Preeti
APPLICANTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
FILE REFERENCE: GX-0019-1 P
CURRENT APPLICATION NUMBER: US/60/324,185
CURRENT EILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOUTWARE: PERL Program
SEQ ID NO 29531
LENGTH: 3814
TYPE: DNA
TYPE: DNA Sequence 29531, Application GENERAL INFORMATION: US/60324185

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; TYPE: DNA
; ORGANISM: HOMO
US-09-834-291-2
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CURRENT EILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 720
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100.0%; Pred. No. 3.3e-144;
7ative 0; Mismatches 0;
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APPLICANT: Hyseq, Inc.
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Best Local
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CURRENT APPLICATION NUMBER: US/09/404,284
CURRENT FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
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ORGANISM: Homo
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 ggcacggaa
                            TCTGGGGAGTGAGGAAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGCACT
                                          CTTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCT
                                                                                                                                                                                                 CTCACCCTGACTTCTCCCCCTCCCTACCCGCGCGCGAGGCCAAGTTGCTGAATCAATGGAG
                                                                                                                                                                                                                                                      CCACTGCAGGAACGCCCCGGGACAGGAATGCCCATTTGTGCAACGAACCCTGACTCCTTC
                                                                                                                                                                                                                                                                                                             AGCCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAAGTGAGCATGCCAG
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426; Conserv
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99.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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GGCACGGGA

US-09-524-038-674/c

Sequence 674, Application US/09524038
GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark C.
APPLICANT: Jones, Lee w.

TITLE OF INVENTION: Novel Nucleic Acid Sequences TITLE OF INVENTION: From Various Libraries FILE REFERENCE: 780CIP

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US-60-324-185-9888/c
; Sequence 9888, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: MORRIS, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Lal, Preeti
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLECTIDE SEQUENCE DATABASES, AND SINGLE NUCLECTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/524,038
CURRENT FILING DATE: 2000-03-13
EARLIER APPLICATION NUMBER: 09/404,284
EARLIER FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hy-Patent.pl Version 3.1
SEQ ID NO 674
LENGTH: 449
TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 1156, 1235, 1267, 1304,
THER INFORMATION: a, t, c, g, or
US-60-324-185-9888
                                                                                                                                                                                                                                                                                                                      Sequence 7725, Application US/09644867 GENERAL INFORMATION:
                                                      SOFTWARE: Fa
SEQ ID NO 7725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 9888
LENGTH: 1368
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                               APPLICANT: Holtzman, Douglas A.
APPLICANT: Donovan, Michael J.
APPLICANT: Leiby, Kevin R.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1173-001
CURRENT APPLICATION NUMBER: US/09/644,867
CURRENT FILING DATE: 2000-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                             PRIOR APPLICATION NUMBER: 60/151,061 PRIOR FILING DATE: 1999-08-27
                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/60/324,185
CURRENT FILING DATE: 2001-99-21
NUMBER OF SEO ID NOS: 35862
SOFTWARE: PERL Program
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                 LENGTH: 1732
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
OTHER_INFORMATION: Incyte ID No: 1383957.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2649 cggaactcctggacaagccctgacaagcc 2677
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Local Similarity 99.7%;
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                                                                        FastSEQ for Windows Version 4.0
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Pred. No. 2.6e-73;
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US-09-644-867-7725

Query Best I Matche	atch 11.5%; Score 367.8; DB 25; Length 1732; cal Similarity 99.5%; Pred. No. 5.3e-69; Indels 0; Ga 369; Conservative 0; Mismatches 2; Indels 0; Ga conservative 0; Mismatches 0; Ga conservative 0; Ga conserva	
Qy 2289 Db 389	9 cocytcttagtcocygygatagycaaaytygygycygygcygygyacygygytycygygattycy 2348 	
Qy 2349	19 gcggcagcggcgcacgcggggcacctgggagcggcggggctgctgcggggaggcgttggagac 2408	
Db 329		
Оу 2409		
Db 269	9 TGGCTCCCGGGGCTGTTAGGACCTTCCCTCAGGCCCGGGTGCTCAGAACGCTGGAGGAC 210	
Qy 2469		
Db 209	)9 TTGCTTTTCTTGGGCCTTGATGCGAAGTGCTGATCCCGCTGGGCAGGCGGGGCAGCTCCG 150	
Qy 2529		
Db 149	9 GCGCTCCTCGGAGACCACTGCGCTCCACGTTGAGGTGGGCGTGGGGGGGCGGACAGGAATT 90	
Qу 2589	99 gaagcggaagtctgggaagctttagggtcgctggagggggacccccggttggagagagggg 2648	
Db 6	89 GAAGCGGAAGCCTGTTAGGGTCGCTGGAGGGGGACCCCGGTTGGAGAGAGGAG 30	
Qy 2649	9 cggaactcctg 2659	
Db	29 CGGAACTCCGG 19	
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Search completed: September 7, 2002, 22:30:49 Job time: 43743 sec

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Post-processing: Minimum Match 0%
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1: /cgn2_6/ptodata/2/pna/U
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3: /cgn2_6/ptodata/2/pna/U
4: /cgn2_6/ptodata/2/pna/U
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6: /cgn2_6/ptodata/2/pna/U
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7: /cgn2_6/ptodata/2/pna/U
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US-10-113-364-477
US-10-143-906-21
PCT-US02-1266-9394
US-10-035-832-1263
US-10-007-926A-143
US-10-035-832-1259
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US-10-113-872-1669
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                                                                                                                                                                               Sequence 1262, Ap
Sequence 674, App
Sequence 477, App
Sequence 21, Appl
Sequence 9394, App
Sequence 1263, Ap
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Sequence 123, App
Sequence 1259, Ap
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1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7
375	375	27827	2759	113585	44990	44990	1076	551	48763	2501	1527	1191139	1191139	443	443	443	443	1140	1140
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PCT-US02-09239-331	PCT-US02-09239-329	US-10-035-832-1328	us-10-027-632-111688	US-10-188-470-12	US-10-052-482-217	US-10-035-832-1229	US-10-098-754-1296	US-10-027-632-71673	PCT-US02-23268-3	US-10-027-632-103140	US-10-011-154-202	US-10-140-924-1	US-09-811-352B-1	us-10-027-632-296991	us-10-027-632-296990	US-10-027-632-64317	US-10-027-632-64316	US-10-027-632-253751	US-10-027-632-253750
Sequence 331, App	Sequence 329, App	Sequence 1328, Ap	Sequence 111688,	Sequence 12, Appl	Sequence 217, App	Sequence 1229, Ap	Sequence 1296, Ap	Sequence 71673, A	Sequence 3, Appli	Sequence 103140,	Sequence 202, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 296991,	Sequence 296990,	Sequence 64317, A	Sequence 64316, A	Sequence 253751,	Sequence 253750,

## ALIGNMENTS

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILLING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 1613

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1262

LENGTH: 45121

TYPE: DNA
ORGANISM: Homo sapiens
US-10-035-832-1262 Sequence 1262, Application US/10035832; GENERAL INFORMATION: US-10-035-832-1262 Query Match
Best Local Similarity
Matches 3207; Conserv APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
CURRENT FILING DATE: 2002-07-22 PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22 8054 tttccccagaacaccagcattcattaggtgttcattcaatagattcttcaaaggattcca 8114 aaggcaaagaagtttggggaacagtatatataattacccaaccctttgacattagcatac 121 181 61 gaacttgaggataattagacgtacgtgggtagagggtagggggaagggggtatggcataga 360 taagggccctgagaagttttggattaagaaagttttcaaaattaaagtaacccagaatttt aaggcaaagaagtttggggaacagtatatataaattacccaaccctttgacattagcatac ctaagattatttgaccatgaaacatatgtctccccacaaagcacatattcctatctctt ctaagattatttgaccatgaaacatatgtctccccacaaagcacatattcctatctcctt 300 taagggccctgagaagttttggattaagaaagttttcaaattaaagtaacccagaatttt Conservative 99.4%; Score 3193; 99.8%; Pred. No. 0; 0; Mismatches DB 6; Length 45121; 5; Indels ۲, Gaps

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1139 9133	1080 ttaatgtgttattaatgggttgaatctaattgggaaggggagagagggttgcagagtgaggt 	В 0
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780 8773	721 attitggaatagtittaggatitcaaaaaattigcagagataatacagagaatgcccata 	
720 8713	661 officectoacacccottffcctfcctfttftacaffftftftatffaatgaacfffftc	
660 8653	601 cotttoccottttttttctctcttccctccttccattccttcttccttacctctcctttc	
600 8593	541 cacatatgtgagttgctggcttataattcacactcaagagatactgattttgtcaattgt	
540 8533	84 4	
480 8473	8 4	
420 8413	8 3 3 3	
8353	Db 8294 gaacttgaggataattagacgtacgtgggtaggggtagggggaagggggtatggcataga	

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US-10-011-154-674/c
CURRENT APPLICATION NUMBER: US/10/011,154
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-13 |
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21 |
NUMBER OF SEQ ID NOS: 4670 |
SOFTWARE: Hy-patent.pl Version 3.1 |
SEQ ID NO 674
                                                                                                                                                                                                                                                                               Sequence 674, Application US/10011154
GENERAL INFORMATION:
                                                                                                                                                                                               APPLICANT: Drmanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark C.
APPLICANT: Jones, Lee w.
                                                                                                                                                  TITLE OF INVENTION: Novel Nucleic Acid Sequences TITLE OF INVENTION: From Various Libraries FILE REFERENCE: 780CIP
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; ORGANISM: Homo sapiens US-10-011-154-674
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                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/179,065
PRIOR ETLING DATE: 2000-01-31
PRIOR EPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                   PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/211,364
CURRENT FILING DATE: 2002-08-05
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 1778
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                       PRIOR
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                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/760,486
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                                                 APPLICATION NUMBER: 60/217,496
FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/215,447
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/218,290
                                                                                                                    APPLICATION NUMBER: 60/225,758
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/220,963
FILING DATE: 2000-07-26
ADDITION NUMBER: 60/220
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Prior Application removed - S
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 772
TYPE: DNA
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US-10-143-906-21
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                                                                                                                                                                                                                                                                                   Sequence 21, Application US/10143906 GENERAL INFORMATION:
                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REPERENCE: PTZ70C1N
CURRENT APPLICATION NUMBER: US/10/143,906
CURRENT FILING DATE: 2002-05-14
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LENGTH: 772
                                                   NAME/KEY: misc_feature
LOCATION: (593)
OTHER INFORMATION: n equals
FEATURE:
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                        NAME/KEY: misc_feature LOCATION: (594)
                                                                                                           FEATURE:
                                                                                                                   ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (593)
OTHER INFORMATION: n equals
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Pred. No. 1.8e-61;
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; LOCATION: (704)
; OTHER INFORMATION: n equals a,t,g,
US-10-143-906-21
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GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Prostate Cancer Expression Profiles
FILE REFERENCE: 9U 206 PCT
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 85
                                                                                                                                                                                                             Matches 252;
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CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/281,732
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/281,731
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/281,731
PRIOR FILING DATE: 2001-04-06
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Best Local
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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99.78;
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RESULT 6
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US-10-035-832-1263
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                                                                                                                       GENERAL INFORMATION:
                                                                                                                                         Sequence 1263, Application US/10035832
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PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 13946
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CURRENT FILING DATE: 2002-08-14
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              APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
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PRIOR APPLICATION NUMBER: US 09/747,377
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FAULK, Ronald
SUN, Hongwei
SASAI, Hitoshi
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; TYPE: DNA; ORGANISM: Homo sapiens US-10-035-832-1263
                                                                                                                                            ; ORGANISM: Homo sapiens ; FEATURE: OTHER INFORMATION: tumor necrosis factor receptor superfamily, ; OTHER INFORMATION: member 6 (TNFRSF6) gene.
US-10-007-926A-143
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NUMBER OF SEQ ID NOS: 1613
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1263
LENGTH: 2551
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LENGTH: 2551
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Best Local Similarity
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APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: FERT, VINCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/254,090 PRIOR FILING DATE: 2000-12-08 NUMBER OF SEQ ID NOS: 468
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/007,926A CURRENT FILING DATE: 2001-12-07
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES FILE REFERENCE: 1546-R-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BERTUCCI, FRANCOIS
                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                          TYPE: DNA
2007 gcaagagtgacacacaggtgttcaaagacgcttctggggagtgagggaagcggtttacga 2066
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Local Similarity 100.0%; Pred. No. 9.4e-44;
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                                                                           100.0%;
                                                                           7.8%; Score 252; DB 7; l00.0%; Pred. No. 9.4e-44;
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APPLICANT: MORTIS, David

APPLICANT: MORTIS, David

APPLICANT: Engelhard, Eric

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

FILE REFERENCE: A-71249/RMS/DCF

CURRENT APPLICATION NUMBER: US/10/035,832

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-03-02
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CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 233
LENGTH: 2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 233, Application US/09053375B GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvilli, Robert
TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CLON-006
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TYPE: DNA
ORGANISM: Homo sapiens
-09-053-375B-233
NUMBER OF
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241 cctacctctggt 252
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SEQ ID NOS:
                                                                                                                                                                                                 Application US/10035832
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US-10-027-632-145670/c; Sequence 145670, App.; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1259
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LOCATION: (55549)..(55568)
OTHER INFORMATION: "n" at positions
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LOCATION: (42691)...(42710)
OTHER INFORMATION: "n" at
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LOCATION: (48271)..(48290)
OTHER INFORMATION: "n" at
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LOCATION: (46987)..(47006)
OTHER INFORMATION: "n" at
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LOCATION: (31023)..(31239)
OTHER_INFORMATION: "n" at positions 31023 thru
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LOCATION: (29253)..(29272)
OTHER INFORMATION: "n" at positions 29253 thru 29272
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ORGANISM: Mus musculus
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RESULT 13
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1090-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C19
CURRENT APPLICATION NUMBER: US/10/113,872
CURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 2011
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 325720
                                                     2374 TAGATTTACAGAGAAGTTGCAGAGATAGTACAAAGAGTTCCTGTATACCCTTCACC 2319
                                                                                                                                    LENGTH: 2435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 816
                                                                         736 taggatttcaaaaaatttgcagagataatacagagaatgcccatataccatcctcc 791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          757 gagataatacagagaatgcccatatacccatcctccttatcccacttctttttgtgtctat 816
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                                                                                                                                                                                                                                 Local Similarity es 81; Conserv
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Local Similarity 69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83;
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Kalos, Michael D.
Sleath, Paul R.
Vedvick, Thomas S.
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; ORGANISM: Human US-10-027-632-91808
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                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILLING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILLING DATE: 1999-08-09
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                            SEQ ID NO 91808
LENGTH: 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 91808, Application US/10027632
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Best Local Similarity 69.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-04-20 PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Carter, Darrick
APPLICANT: Franger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C19
CURRENT FILING DATE: 2002-03-28
CURRENT FILING DATE: 2002-03-28
CURRENT FILING DATE: 2002-03-28
CURRENT FILING DATE: 2002-03-28
COURSER OF SEQ ID NOS: 2011
                                                   LENGTH: 54
TYPE: DNA
                                                                                                                                  SOFTWARE:
                                                                                                                                                           NUMBER OF SEQ ID NOS:
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Kalos, Michael D.
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Best Local Similarity Matches 70; Conserv

Conservative

1.8%; Score 59.2; DB 7; 79.5%; Pred. No. 0.0081; ative 0; Mismatches 18;

DB 7; Length 542;

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0;

Query Match

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US-10-027-632-304597
US-10-027-632-304597
Sequence 304597, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION. Identification and Mapping of Single Nucleotide
TITLE OF INVENTION. Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-8
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-8
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: US 60/167,363
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; ORGANISM: Human
US-10-027-632-304597
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Best Local Similarity 79.5%;
Matches 70; Conservative (
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Title:
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and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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BG659530 TgESTzya2
BF569266 602185634
BG121070 602352793
AV695647 AV695647
AA05863 zf55b04.s
AA047220 zf49e11.s
AA057218 zf59h03.s
AA047220 zf49e17.s
AA02092 ze65f07.s
AA02092 ze65f07.s
H84228 ys95e09.s1
H84228 ys95e09.s1
AW339285 xb38d02.y
AA018441 ze50a08.s
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62.8	63	63	63.2	63.4	63.6	63.6	63.6	63.8	65.2	66	66.4	67	80.4	96	114.4	124.4	135	181.8	185.2	190	191	202.4	210.4	214	214.4	215.4	253
2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.1	2.1	2.1	2.5	3.0	3. 6	ω. 9	4.2	5.7	5.8	5.9	5.9	6.3	6.6	6.7	6.7	6.7	7.9
987	1201	698	1101	699	583	549	306	1027	932	1101	993	1101	1101	285	341	291	577	828	696	419	800	1052	300	932	1339	359	381
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CNS016F1	CNS0165X	AZ184604	CNS0182P	BG076530	AA521406	AA521324	AA668797	CNS016J7	CNS0072Q	CNS01523	AG090948	CNS0039G	CNS0039G	вм090262	AA375635	AA383161	BM310113	в1838027	AV715411	R85827	BI463384	BM455788	AU100132	AL542093	BG288747	AV692383	H86544
AL106663 Drosophil	AL106335 Drosophil	AZ184604 SP_1003_A	ALIUSBII Drosophii	BG076530 H3001D05-	AA521406 aa68C09.S	AA521324 aa68eU9.s	AA668797 aa80dll.s	ALIU6813 Drosophii	AL066742 Drosophia	AL104901 Drosophii	AG090948 Pan trogi	AL063921 Drosophii	AL063921 Drosophil	BM090262 505440 MA		AA383161 EST96716	BM310113 inlinit.y		AV715411 AV715411	R85827 yq22g10.s1	BI463384 603204413	BM455788 AGENCOURT	DIOOTS	AL542093 AL542093	BG288/4/ 502385555	AV692383 AV692383	H86544 YTU4TUL.SI

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## ALIGNMENTS

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	FEATURES source		REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 B1763679/c LOCUS DEFINITION
/Ob_xref="taxon:9606" /db_xref="taxon:9606" /clone="IMAGE:5189752" /clone=lib="NIH_MGC_116" /clone=lib="NIH_MGC_116" /lab_host="Deled colon, kidney, stomach; Vector: /note="Organ: pooled colon, kidney, stomach; A9 yo source anonymous pool of 3 colons, age 26 yo male, 49 yo source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is	Plate: LLA High quali I	Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	nammalia, Bulletia, Frances, Constant, Manualian (MGC) 1 (bases 1 to 793) 1 (bases 1 to 793) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.	BI763679 BI763679.1 GI:15755257 EST. human. human. Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.	B1763679 793 bp mRNA linear EST 25-SEP-2001 603049567F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189752 5',

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Pred. No. 3.5e-115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          694 acattttttatttaatttaaatgaacttttcatttttggaatagttttaggatttcaaaaaattt 753
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agtgcagtgacagatgcaaaacacagggtgatggaaagccctcaggagggtaacctaacc
                                                                                                                       GCAGAGATAATACAGAGAATGCCCATATACCATCCTCCTTATCCCACTTCTTTTTGTGTC 120
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Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE Consortium (info@image.llnl.gov) for Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 459.
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4444 Forest Park Parkway, Box 8501, St. Louis,
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clone IMAGE:450771 3', mRNA sequence.
AA704610
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Fax: 314 286 1810
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/lab_host="DH10B (ampicillin resistant)"
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/clone="IMAGE:450771"
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Pred. No. 5.5e-70;
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2469 ttgcttttcttgggccttgatgcgaagtgctgatcccgctgggcqggcggggcagctccg
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                                                                                                                                                                                                 400 CCCGTCTTAGTCCCGGGGATAGGCCAAAGTGGGGCGGGC-CGGGACGCGTGCGGGATTGCG
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                                                                                                                      GCGGCAGCGGCACCCGGGCACCTGGGAGCGGGGGGGCTGCTGCGGGAGGCGTTGGARAC
                                                                                                                                    gcggcagcggcgcacgcgggcacctgggagcgggctgctgctgcgggaggcgttggagac
                                          TGGCTCCCGGGGGCTKTTAGGACCTTCCCTCAGGCCCGGGTGCTCAGAACGCTGGAGGAC
                                                               tggctcccgggggctgttaggaccttccctcaggcccgggtgctcagaacgatggaggac
                                                                                                                                                                                                                                                                               397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="organ: placenta; Vector: pcMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was constructed by Life pcMVSPORT 6 vector. Fibrary was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                 fliang@lifetech.com URL :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxoplasma EST Project
Toxoplasma EST Project
Washington University School of Medicine
Washington University School of Medicine
January Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                           Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seg primer: -40RP from Gibco High quality sequence stop: 371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, Tel: 314 286 1800 Fax: 314 286 1810 Email: toxo@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
Contact: Clifton, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxoplasma EST Project
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Location/Qualifiers
                  86 a
                                                                     cells
                                                  a small percentage contaminants from human
                                                                                                                                                                                                                                                               /clone="TgESTzya24g01.y1"
/clone_lib="TgVEG118 Tachyzoite cDNA Library"
/dev_stage="Tachyzoite"
                                                                                                                                                                                                                                                                                                                                        /organism="Toxoplasma gondii"
/strain="VEG"
                                                                                                                                                                                                                                                  /lab_host="DH10B"
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                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLCM1184 row: c column: 10
                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Linehan
                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
national Institutes of Health, Mammalian Gene
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602185634F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309953
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                        quality sequence stop: 595.
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/clone_lib="NIH_MGC_45"
/tissue_type="renal carcinoma (ascites)"
/lab_host-"DH10B (phage-resistant)"
/note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California,
                                                                                                                                                  /clone="IMAGE:4309953"
                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                       found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov http://image.llnl.gov i column: 24
                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1140)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                 602352793F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4451039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1
                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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BG121070
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/db_xref="taxon:9606"
              /organism="Homo sapiens"
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                                                                                                                                                        Xi,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                   351 Guo Shoujing Road, Zhangjiang Hi-Tech
201203, p. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Verțebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 617)
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AV695647 GKC Homo sapiens cDNA clone GKCFCD11 5', mRNA sequence.
AV695647.1 GI:10297510
                                                                                                    Contact: Zeguang Han
Chinese National Hum
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Email: hanzg@chgc.sh.cn
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/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHLMGC Library."
a 342 c 331 g 178 t
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/tissue_type="adenocarcinoma, cell| line"
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Local Similarity 98.0%;
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zf55b04.sl Soares retina N2b4HR
IMAGE:380815 3', mRNA secuence
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                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. J
                                                                                  Contact: Wilson RK
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/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
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/db_xref="taxon:9606"
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1. .617
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Pred. No. 6.1e-48;
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                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 577)
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins, M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
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/clone="IMAGE:380815"
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/db_xref="GDB:1289072"
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99.7%;
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zf49e11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380300 3', mRNA sequence.
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Location/Qualifiers
1. .577
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Contact: Wilson RK
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The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40M13 fwd. from Amersham
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/lab_host="DH10B (ampicillin resistant)"
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/dev_stage="55 year o
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/db_xref="GDB:1288949"
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1. (bases 1 to 547)
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128 c 125 g 158 t
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/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
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/clone="IMAGE:380300"
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/db_xref="GDB:1288557"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares retina N2b4HR"
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                                                                                                                                                                                                                                                                   8.7%;
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                                                                                                                                                                                                                                                                   Score 280.4; DB 9
Pred. No. 1.6e-39;
                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                   DB 9; | Length 547;
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망 Ω<sub>γ</sub>

1 GTCNCACAGAAAAAGAAACTGCCTTGTCTCCCTTCCGGGAATTCTCTCTTTAAGACTNGT 60

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SOURCE
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                                                            Local Similarity
                                             291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA011028 442 bp mRNA linear EST ze34d02.sl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360867 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 844
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314 286 1810
                                             Conservative
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                                                                                                                                                       Soares and M.Fatima Bonaldo.
1 107 c 103 g 138 t
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                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="retina"
/dev_stage="55 year old"
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/clone="IMAGE:360867"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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                                                            Score 279.4; DB 9
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                                                                            Length 442;
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                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Lé, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. The Washu-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 447)
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                 95
                                                                                                                                                                                                                                                                                                                                         quality sequence stop:
Location/Qualifiers
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B1269 3', mRNA sequence.
     Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                     /db_xref="GDB:1289526"
/db_xref="taxon:9606"
/clone="IMAGE:381269"
                                                                                                                                                                                                                  /tissue_type="retina"
/dev_stage="55 year o
                                                                                                                                                                                                                                              /sex="male"
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Hiller J. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellanberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M., Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                      FMAX: 314 400 ---- Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School
4444 Forest Park Parkway, Boy
                                                                                                                                                                                                                                                                                 Seq primer: -40Ml3 fwd.
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AA020992.1 GI:1484745
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/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="0H10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT7T3D (Pharmacia)
modified polylinker; Site_1: Not I; Site_2: Ec
                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:1280580"
/db_xref="taxon:9606"
/clone="IMAGE:363877"
                                                                                                            /sex="male"
                                                                                                                          /clone_lib="Soares retina N2b4HR"
                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 bp mRNA linear EST Soares retina N2b4HR Homo sapiens cDNA clone 77 3' similar to contains Alu repetitive eleme
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98.6%;
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Pred. No. 3.6e-39;
                                                                                                                                                                                                                                                                                 from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                      of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mardis, E., Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 30-JAN-1997
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                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                           TITLE
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                                                                                                                                                                                                                                                               AUTHORS
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3160 gttttgaaaagtccctcgctcagaaatgccagcttgca 3197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3100 tactcgttcccaccgcacagaacccggcgcctattattggcccaagaaacttgagcagcct 3159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACTCGTTCCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277;
                                                                                                                                                                                      Email: est@watson.wustl.edu
High quality sequence stops: 364
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 881 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                       376 bp
ys95e09.s1 Soares retina N2b5HR
IMAGE:222568 3', mRNA sequence.
H84298
                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                              Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                           Seq primer: Promega -21ml3
                                                                                                                                                                                                                                                                                                                    Homo sapiens
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quality sequence stop: 364.
Location/Qualifiers
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                                                     further information
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H84298 RESULT

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                                                                                                                                             AUTHORS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctattattggccaagaaacttgagcagcctgttttgaaaagtccctcgctcagaaatgcc 3189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTTCCCACCGCACAGAACCCGGCGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTTTTCTGCCCTTCTTCTTTTTTTGCCCTTTCTTAGCTTGCACTCCCATGGTGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCTTGCAGATGGCTAATCAAAG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263;
                                                     1 (bases 1 to 398)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The WashU-Merck EST Project
                     Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                               H86126 398 bp mRNA linear EST ys94g08.s1 Soares retina N2b5HR Homo sapiens cDNA clone
Washington University School of Medicine
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                        H86126.1 GI:1067705
                                                                                                                                                                                                                                                                                                                            IMAGE: 222494 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTTT3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="retina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares retina N2b5HR"
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/clone="IMAGE:222568"
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/db_xref="GDB:3851329"
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100.0%; Pred. No. 1.9e-36;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                   mRNA
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FEATURES
                                                                                                                                                                                                                                                                            Query Match 8.0%;
Best Local Similarity 99.6%;
                                                                                                                                                                                                                                                                Matches 268;
                                                   3185 atgccagcttgca-gatggctaatcaaag 3212
                                                                                                                   3065 gtgatttctgcttggtctccctgctggggtttggtactcgttcccaccgcacagaaccc 3124
                                                                                                                                                                      3005 tgttttgtttttctgcccttctcttttcttctttttgccctttcttagcttgcactcccatg 3064
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                                                                                                       121
                                                                                                                                                          61 TGTTTTGTTTTTCTGCCCTTCTCTTTCTTTTTTGCCCTTTCTTAGCTTGCACTCCCATG 120
                                                                                                                                                                                                              1 GTCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTCATTT 60
ATGCCAGCTTGCAGGATGGCTAATCAAAG 269
                                                                                                       GTGATTTCTGCTTGGTCTCCTGCTGGGGGTTGGTGGTACTCGTTCCCACCGCACAGAACCC 180
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/db_xref="cDB:3851255"
/db_xref="taxon:9606"
/clone="IMAGE:222494"
/clone_lib="Soares retina N2b5HR"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                            Score 257; DB 10; Length 398; Pred. No. 2.1e-35;
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Search completed: September Job time: 16175 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/2/pna/P

2: /cgn2_6/ptodata/2/pna/U

3: /cgn2_6/ptodata/2/pna/U

4: /cgn2_6/ptodata/2/pna/U

5: /cgn2_6/ptodata/2/pna/U

6: /cgn2_6/ptodata/2/pna/U

6: /cgn2_6/ptodata/2/pna/U

8: /cgn2_6/ptodata/2/pna/U
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    September 8, 2002, 01:10:14; Search time 1826.34 Seconds (without alignments) 208.437 Million cell updates/sec
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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US-10-137-113-12

US-09-918-995-29556

US-10-211-625-47

US-09-646-569-178

US-09-646-569-178

US-09-646-569-178

PCT-US02-18947-329

US-10-172-118-329

US-10-1018-311A-1

US-09-919-002-3827

PCT-US02-23766-4

US-10-205-951-4

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US-10-205-951-4

US-10-205-951-1

US-10-205-303-558

US-10-158-034-107
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PCT-US02-25766-3153
US-10-018-407A-1
PCT-US02-23766-55
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                   Sequence 1262, Ap Sequence 1, Appli Sequence 1, Appli Sequence 12, Appl Sequence 17, Appl Sequence 1, Appl Sequence 15, Appl Sequence 558, Appl Sequence 558, Appl Sequence 17, Appl Sequence 27, Appl Sequ
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30.2	30.6	30.8	30.8	30.8	30.8	30.8	30.8	30.8	31	31	31	31	31.2	31.2	31.2	31.4	31.6	31.6	31.8	
24.2	24.5	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.8	24.8	24.8	24.8	25.0	25.0	25.0	25.1	25.3	25.3	25.4	
17235	2056	16000	5055	5054	5054	5054	1062	1062	1891	1374	790	517	1552	1371	643	502	2439	1748	421	
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US-10-201-255-206	US-09-994-404-70	PCT-US02-22630-12	PCT-US02-22630-3	US-10-172-118-445	US-10-007-926A-428	PCT-US02-18947-445	US-09-053-375B-1377	US-08-134-231B-33	US-10-205-267-2	US-09-919-002-4023	US-10-027-632-169978	US-10-205-267-4	PCT-US02-25107-37	US-10-198-846-9726	PCT-US02-25107-20	US-09-918-995-32522	US-10-198-846-13296	PCT-US02-25766-8269	US-09-721-544-21692	
Sequence 206, App	Sequence /U, Appl	Sequence 12, Appl	Sequence 3, Appli	Sequence 445, App	Sequence 428, App	Sequence 445, App	Sequence 1377, Ap	Sequence 33, Appl	Sequence 2, Appli	Sequence 4023, Ap	Sequence 169978,	Sequence 4, Appli	Sequence 37, Appl	Sequence 9726, Ap	Sequence 20, Appl	Sequence 32522, A	Sequence 13296, A	Sequence 8269, Ap	Sequence 21692, A	

## ALIGNMENTS

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APPLICANT: MORFIS, David
APPLICANT: MORFIS, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILLING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILLING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: Patentin version 3.1
SEQ ID NO 1262
LENGTH: 45121
TYPE: DNA
ORGANISM: Homo sapiens
US-10-035-832-1262
  PCT-US02-25766-3153

; Sequence 3153, Application PC/TUS0225766
; GENERAL INFORMATION:
; APPLICANT: GENE LOGIC, INC.
; APPLICANT: MUNGER, William E
; APPLICANT: FAULK, Ronald
: APPLICANT: FAULK, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-10-035-832-1262
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Best Local Similarity
Matches 125; Conserv
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APPLICANT:
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                                                                                                                                                                                                                                                                                   121 tggag 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gatcccgctgggcaggcggggcagctcctcggcgctcctcggagaccactgcgctccacgtt 60
SUN, Hongwei
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100.0%; Pred. No. 3e-22;
tive 0; Mismatches 0;
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PCT-US02-23766-55/c
|: Sequence 55, Appl
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SEQ ID NO 1
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Best Local Similarity 58.9
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APPLICANY: C. Frank Bennett
APPLICANY: Lex M. Cowsert
APPLICANY: ISIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-2 EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/311,837
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 13946
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3153
LENGTH: 4657
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CURRENT APPLICATION NUMBER: US/10/018,407A
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 09/339,964
PRIOR FILING DATE: 1999-06-25
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: PCT/US02/25766
CURRENT FILING DATE: 2002-08-14
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TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
FILE REFERENCE: 44921-5068-WO
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (212)..(3988)
                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                     4408 ggtggggggggtgtccgtccggaaatgaaggaatagcccgaggacc 4454
                                                                                                                                                        4348 ttccaccgggcctgaaccacagcggaggagctccgctaagacctccccacccccgctggg 4407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4322 ggtggggggggtgtccgtccggaaatgaaggaatagcccgaggacc 4368
                                                                                                      63 ggtgggcgtggggggggaaggaattgaagcggaagtctgggaagc 109
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63; Conserv
Application PC/TUS0223766
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58.9%;
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58.9%;
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Pred. No. 2.9;
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Pred. No. 2.9;
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US-10-137-113-12/c

: Sequence 12, Application US/10137113

: GENERAL INFORMATION:
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; ORGANISM: Human
US-10-205-951-55
                                                                                                                                                       RESULT
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APPLICANT: Le, Wei-dong
APPLICANT: Vassilatis, Demetrios K
TITLE OF INVENTION: Mutant Nurrl Gene in Parkinson's Disease
FILE REFERENCE: P02512W01
CURRENT APPLICATION NUMBER: PCT/US02/23766
CURRENT FILING DATE: 2002-07-26
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APPLICANT: Bannantine, John P. TITLE OF INVENTION: Mycobacterial Diagnostics FILE REFERENCE: 09531-112001
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Best Local Similarity 60.2%;
                                                               APPLICANT: Kepur, Vivek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/205,951
CURRENT FILING DATE: 2002-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Mutant Nurr1 Gene in Parkinson's Disease FILE REFERENCE: P02512US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/308,294
PRIOR FILING DATE: 2001-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Le, Wei-dong APPLICANT: Vassilatis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: US 60/308,294
PRIOR FILING DATE: 2001-07-27
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ORGANISM: Human
                                                                                                                                                                                                                                                                                               5688 GCAGGGCAGCTTCGGCGGACCCCGGAGAGCTGGGCAGTCCCGGGAGAGCTGGGGCTGGGC 5629
                                                                                                                                                                                                                5628 TACTGGCACCAAGGCAGAGGGCACACTCCGAGG 5596
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                                                                                                                                                                                                                                                                                                                                                                           27.0%;
Local Similarity 60.2%;
les 56; Conserva+***
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                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.8;
Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                37; Indels
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CURRENT APPLICATION NUMBER: US/10/137,113
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/362,396
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Mycobacterium paratuberculosis
US-10-137-113-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 199-01-20
NUMBER OF SEQ ID NOS: 38054
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-918-995-29556/c ; Sequence 29556, Application US/09918995 ; GENERAL INFORMATION:
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; LCCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-29556
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Sequence 47, Application US, AVELON ESQUENCE 47, Application US, AVELON ENGINE REPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PM034CIN
CURRENT APPLICATION NUMBER: US/10/211,625
CURRENT APPLICATION NUMBER: US/10/211,625
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                   453 GGTGGGGAAGGTGGAGGGCTGGCAGCAGCCCCAGCGCTTGAGTTGGGGGGTCGGCCTCGG 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Match 26.6%; Local Similarity 64.1%; nes 50; Conservative
                                                                                                                                                                                                                                                                                393 GGACGGGCCTGGGTGAAGGGCAGGCCTGGGA 362
                                                                                                                                                                                                                                                                                                                75 gggcggacaggaattgaagcggaagtctggga 106
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59.8%;
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Pred. No. 21;
0; Mismatches 28;
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Pred. No. 27;
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; ORGANISM: Homo sapiens US-09-646-569-178
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                                    SOFTWARE: PatentIn Ver.
SEQ ID NO 178
LENGTH: 3265
TYPE: DNA
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PRIOR TILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 66/179,065
PRIOR FILING DATE: 2000-01-31
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                                                                                                                                                                                                                                                  APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BREAST TISSUE
FILE REFERENCE: ALBRE 8
                                                                                                                PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: DE 198 13 835.0
PRIOR FILING DATE: 1998-03-20
NUMBER OF SEQ ID NOS: 210
                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/646,569
CURRENT FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: PCT/DE99/00909
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LOCATION: (2109)
OTHER INFORMATION: n equals a,t,
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LOCATION: (2113)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 ggcggggcagctccggcgctcctcggagaccactgcgctccacgttgaggtgggcgtggg 74
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SCHMITT, ARMIN
PILARSKY, CHRISTIAN
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Pred. No. 26;
0; Mismatches
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; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 178
; LENGTH: 3265
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-646-569A-178
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                                                                             SEQ ID NO 329
LENGTH: 3656
                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Rosetta Inpharmatics
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-228
                                                                                                                                                                                                                                                                                             Sequence 329, Application PC/TUS0218947
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APPLICANT: SPECHT, THOMAS
APPLICANT: HINZMANN, BERN
APPLICANT: SCHMITT, ARMII
APPLICANT: PILARSKY, CHRI
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Best Local :
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                                                                                                              CURRENT APPLICATION NUMBER: PCT/US02/18947
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
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                    TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/646,569A

CURRENT FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: PCT/DE99/0099

PRIOR APPLICATION NUMBER: DE 198 13 835.0

PRIOR FILING DATE: 1998-03-20

NUMBER OF SEQ ID NOS: 210

NUMBER OF SEQ ID NOS: 210

NUMBER OF SEQ ID NOS: 210

NUMBER OF SEQ ID NOS: 210
DATABASE ACCESSION NUMBER: AL137555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 tgggaacgaggtgcagatcctgagcaacctggtgatggaggagctgggccctgagctgaa 239
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                                                                                                                                                                                                                                                                                                                                                                                                              69 cgtggggggggggacaggaattgaagcggaagtcttgggaagctttagggttcgctgga 124
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SCHMITT, ARMIN
PILARSKY, CHRIST
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Pred. No. 26;
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Pred. No. 26;
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US-10-018-311A-1
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US-10-172-118-329
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                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                         Sequence 1, Application US/10018311A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Pete
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 329
LENGTH: 3656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                      CURRENT APPLICATION NUMBER: US/10/018,311A CURRENT FILING DATE: 2002-04-19 NUMBER OF SEQ ID NOS: 8
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                                                                                                                     APPLICANT: MIYATA, TOShio
APPLICANT: KUROKAWA, Kiyoshi
TITLE OF INVENTION: Meg 3 protein
FILE REFERENCE: 2605/101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
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Best Local Similarity
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APPLICANT:
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/172,118

CURRENT FILING DATE: 2002-06-14

PRIOR APPLICATION NUMBER: 60/380,770

PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 2699
LENGTH: 3768
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                                                                                                                                                                                                                                                                                                                          601 ggcagagctcggcccgcggctgaaggggaaaccgcaggagcggcagcggcagtgga 656
                                                                                                                                                                                                                                                                                                                                                                                                          541 tgggaacgaggtgcagatcctgagcaacctggtgatggaggagctgggccctgagctgaa 600
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                                                                                                                                                                                                                                                                                                                                                69 cgtggggggggggacaggaattgaagcggaagtctgggaagctttagggtcgctgga 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 26.2%;
Local Similarity 55.2%;
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Van de Vijver, Marc
Bernards, Rene
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Mao, Mao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roberts, Chris
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Pred. No. 25;
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Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Breast Cancer Patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
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PCT-US02-23766-1/c
Sequence 1, Application PC/TUS0223766
GENERAL INFORMATION:
APPLICANT: Le, Wel-dong
APPLICANT: Vassilatis, Demetrios K
TITLE OF INVENTION: MULTAIT Gene in Parkinson's Disease
FILE REFERENCE: P02512W01
CURRENT APPLICATION NUMBER: PCT/US02/23766
CURRENT APPLICATION NUMBER: PCT/US02/23766
PRIOR APPLICATION UNMER: US 66/308,294
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Date of PARCE 2011-07-27
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                                                                                                                                                                                                                                                                                                            RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-919-002-3827; Sequence 3827, Application US/09919002; GENERAL INFORMATION:
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NAME/KEY: misc_feature

LOCATION: 3395, 3437, and 3440

OTHER INFORMATION: N=G,A,C or T
US-10-018-311A-1
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SEQ ID NO 3827
LENGTH: 7318
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Best Local 9
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FILE REFERENCE: 20411-7520N1

CURRENT APPLICATION NUMBER: US/09/919,002

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922

PRIOR FILING DATE: FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/034,341

PRIOR PILICATION NUMBER: APPLICATION NUMBER: US 09/034,341

PRIOR FILING DATE: FILING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 13203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Leshkowitz, Dena APPLICANT: Liu, Jin
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        1165 ggacggggcctgggtgaagggcaggcctggga 1196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 59.8 nes 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64; Conservative
PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.2%; Score 32.8;
59.8%; Pred. No. 25;
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Best Local 9
                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: (1)..(9824) OTHER INFORMATION: n = unknown
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                    4563 GCAGGGCAGCTTCGGCGGACCCCGGAGAGCTGGGGCAGTCCCGGGAGAGCTGGGGCTGGGC 4504
4503 TACTGGCACCAAGGCAGAGGGCACANTCCGAGG 4471
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 9824
                                                                                       16 goggggcagctccgggcgctcctcggagaccactgcgctccacgttgaggtgggcgtgggg 75
                              76 ggcggacaggaattgaagcggaagtctgggaag 108
                                                                                                                                        26.2%;
Local Similarity 59.1%;
hes 55; Conservation
                                                                                                                                            0; Mismatches
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Search completed: September Job time: 37099 sec

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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               September 7, 2002, 22:32:03; Search time 13836.9 Seconds (without alignments) 195.445 Million cell updates/sec
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125
Cgn2_6/ptodata/2/pna/US06_COMB.seq:*

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the number of results predicted by chance to h	ta/2/pna/US( ta/2/pna/US(	_6/ptodata/2/pna/US6034_COMB.seq	_6/ptodata/2/pna/US6033_ _6/ptodata/2/pna/US6033_	_6/ptodata/2/pna/US6031_COMB.seq	_6/ptodata/2/pna/US6030_COMB.s	_6/ptodata/2/pna/US6029_COMB.	6/ptodata/2/pna/US6028_COMB.seq	_o/ptodata/2/pna	_6/ptodata/2/pna/US6025_COMB.seg	_6/ptodata/2/pna/US6024_COMB.seq	_6/ptodata/2/pna/US6023_	_6/ptodata/2/pna/US6022_COMB.	_6/ptodata/2/pna/US6021_COMB.	_6/ptodata/2/pna/US6020_COMB.	_6/ptodata/2/pna/US6019_COMB.s	_6/ptodata/2/pna/US6018_COMB.	_6/ptodata/2/pna/US6017_COMB.	_6/ptodata/2/pna/US6016_COMB.	_6/ptodata/2/pna/US6015_COMB.	_6/ptodata/2/pna/US6014_COMB.	_6/ptodata/2/pna/US6013_COMB.s	_6/ptodata/2/pna/US6012_COMB.	_6/ptodata/2/pna/US6011_COMB.	_6/ptodata/2/pna/US6010_COMB.s	_6/ptodata/2/pna/US6009_COMB.s	_6/ptodata/2/pna/US6008_COMB.s	_6/ptodata/2/pna/US6007_COMB.s	6/ptodata/2/pna/US6006_COMB.se	_6/ptodata/2/pna/US600	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Result 0 0 0 0 0 0 0 0 0 ö 4 5 6 7 7 10 11 11 13 125 125 125 125 123.4 123.4 1123.4 1123.8 121.8 121.8 121.8 121.8 121.8 121.8 121.8 121.8 121.8 121.8 121.8 Score 89.2 89.2 89.2 89.2 85.2 85.3 Match 100.0 100.0 100.0 Query Length DB IJ SUMMARIES Description Sequence 7725, Ap Sequence 10283, A Sequence 11, Appl Sequence 818, App Sequence 818, App Sequence 818, App Sequence 3315, Ap Sequence 3927, Ap Sequence 3927, Ap Sequence 4924, Appl Sequence 4924, Appl Sequence 847, Appl Sequence 847, Appl Sequence 8181, Ap Sequence 8181, Ap Sequence 7672, Ap Sequence 7672, Ap Sequence 7672, Ap Sequence 12154, A Sequence 12154, A Sequence 12154, A Sequence 24990, A Sequence Sequence Sequence Sequence Sequence 9888, Ap 7725, Ap 10283, A 2, Appli Appl

Gaps

0;

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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
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                                                                                                                                                                                                                     Sequence 2780, Application US/09652127 GENERAL INFORMATION:
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Best Local Similarity
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SOFTWARE: PATENTIN VER. 2.1
SEQ ID NO 32
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/09834291 GENERAL INFORMATION:
                                  CURRENT APPLICATION NUMBER: US/09/652,127
CURRENT FILLING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,134
PRIOR FILING DATE: 1999-08-30
                                                                                                                           APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: MOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1183-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
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US-69-339-397-1798
US-60-172-373-10226
US-09-652-128-9418
US-09-36-350A-34407
US-09-359-667-35264
US-09-359-667-36229
US-09-352-510A-36229
US-09-352-65-1176
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e 10226, Ap
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a 34407, A
a 35264, A
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a 35265, Ap
a 1176, Ap
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; SEQ ID NO 2780
; LENGTH: 318
; TYPE: DNA
; ORCANISM: Homo sapiens
US-09-652-127-2780
                     RESULT 4
US-09-834-291-2
: Sequence 2, Application US/09834291
; GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4122
LENGTH: 324
TYPE: DNA
ORGANIZM: Homo sapiens
US-09-396-087-4122
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Best Local :
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TITLE OF INVENTION: PULMONARY ARTERY SMOOTH MUSCLE LIBRARY
FILE REFERENCE: MLN98-39bm
CURRENT APPLICATION NUMBER: US/09/396,087
CURRENT FILING DATE: 1999-09-14
EARLIER APPLICATION NUMBER: 60/100,260
EARLIER FILING DATE: 1998-09-14
EARLIER FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: 60/107,226
EARLIER APPLICATION NUMBER: 60/131,810
EARLIER APPLICATION NUMBER: 60/131,810
EARLIER FILING DATE: 1999-04-30
EARLIER FILING DATE: 1999-04-30
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Best Local Similarity
Matches 125; Conserv
APPLICANT: Krammer, Peter
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: LOCATION: 1156, 1235, 1267, 1304, 1364
: OTHER INFORMATION: a, t, c, g, or other
US-60-324-185-9888
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US-60-324-185-9888/c
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US-09-834-291-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING TITLE OF INVENTION: POLYMUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY FILE REFERENCE: GX-0019-1 P CURRENT APPLICATION NUMBER: US/60/324,185
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL PROGRAM
SEQ ID NO 9888
LENGTH: 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9888, Application US/60324185 GENERAL INFORMATION:
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LENGTH: 720
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Best Local Similarity 100.0%; P
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
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APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
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                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 1383957.6
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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61 gaggtgggcgtgggggggggacaggaattgaagcggaagtctgggaagctttagggtcgc 120
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                                                                     1 gatcecgctgggcaggcggggcagctcctcggggggagaccacctcccacgtt 60
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100.0%; Pred. No. 2.8e-21;
tive 0; Mismatches 0;
                                                                                                                                     Score 125; DB 71;
Pred. No. 2.9e-21;
); Mismatches 0;
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                                                                                                                                                                                Length 1368;
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; ORGANISM: Homo sapiens
US-09-644-867-7725
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                                                                                                    ; TYPE: DNA; Homo sapiens US-09-652-911-10283
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LENGTH: 1732
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SEQ ID NO 10283
LENGTH: 1732
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/644,867
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,061
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 8090
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Query Match
Best Local Similarity
Matches 125; Conserv
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                                                                                                                                                                                                                                               CURRENT FILING DATE: 2000-08-31 PRIOR APPLICATION NUMBER: 60/152,106 PRIOR FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                        APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1190-001
CURRENT APPLICATION NUMBER: US/09/652,911
CURRENT FILING DATE: 2000-08-31
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
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100.0%; Score 125; DB 25; 100.0%; Pred. No. 2.9e-21; O. Mismatches 0;
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                                         Length 1732;
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
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SEQ ID NO 10
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LENGTH: 3212
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                                   PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
                                                                                                                                                              APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCF
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                                                                                                                             CURRENT APPLICATION NUMBER: US/09/997,722 CURRENT FILING DATE: 2001-11-30
                                                                                                                                                                                                           APPLICANT: Morris, David APPLICANT: Engelhard, Es
                 SOFTWARE: PatentIn version 3.1
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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ORGANISM: Homo Sapiens
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125; Conservative
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Pred. No. 2.9e-21;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-036-818
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SOFTWARE: Hy-patent.pl Version 3.1 SEQ ID NO 818
                                                                                                                                                                                                                                     GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 35324
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 818
                                   APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained

TITLE OF INVENTION: From Various Libraries

FILE REFERENCE: 783

CURRENT APPLICATION NUMBER: US/09/943,143

CURRENT FILING DATE: 2001-08-30

PRIOR APPLICATION NUMBER: 09/489,036

PRIOR FILING DATE: 2000-01-19

NUMBER OF SEQ ID NOS: 35324
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APPLICANT: Hyseq, Inc.
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Best Local Similarity
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Best Local :
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99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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NAME/KEY: misc_feature
LCATION: (465)...(578)
THER INFORMATION: similar to gi178067 in the genepept database release 114,
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-471-275-3315
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                                                                                                                                                               SOFTWARE: pt_C
SEQ ID NO 3315
LENGTH: 575
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Best Local Similarity
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EARLIER
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EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: US 09/240,371
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: US 09/277,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Novel Contigs Obtained TITLE OF INVENTION: From Various Libraries FILE REFERENCE: 782
                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: US 09/399,720
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: US 09/404,284
EARLIER FILING DATE: 1999-09-21
                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
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                                                                                                                      ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1999-03-25
APPLICATION NUMBER: US 09/271,490
FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/306,350 FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/125,453
FILING DATE: 1999-03-19
APPLICATION NUMBER: US 60/126,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1999-04-15
APPLICATION NUMBER: US 09/274,861
FILING DATE: 1999-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1999-03-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/293,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/471,275
                                                                                                                                                                                                        _CT_genes Version 1.0
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99.2%;
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Pred. No. 7.1e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-759CON1
CURRENT APPLICATION NUMBER: US/09/362,510
                                     SEQ ID NO 3927
LENGTH: 404
                                                                                                                                                       APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: MOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-759CON1
CURRENT APPLICATION NUMBER: US/09/362,510A
CURRENT FILING DATE: 1999-07-27
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Best Local Similarity
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                                                                            NUMBER OF SEQ ID NOS: 62165
SOFTWARE: FastSEQ for Windows Version
                                                                                                                  PRIOR APPLICATION NUMBER: US 09/221,820 PRIOR FILING DATE: 1998-12-30
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EARLIER APPLICATION NUMBER: US 09/221,820
EARLIER FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 62165
SOFTWARE: FRESTSEQ for Windows Version 3.0
ORGANISM: Homo sapiens
                    TYPE:
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99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Pred. No. 7.1e-21;
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US-09-362-510A-3927

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RESULT 15
US-09-904-013-3927/c
US-09-904-013-3927/c
Sequence 3927, Application US/09904013
GENERAL INFORMATION:
APPLICANY: Hyseq, Inc.
FITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-759CON1
CURRENT APPLICATION NUMBER: US/09/904,013
CURRENT ETLING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/362,510
PRIOR APPLICATION NUMBER: US 09/221,820
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 62165
SOCTUMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3927
LENGTH: 404
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Search completed: September 7, 2002, 22:32:06 Job time: 43820 sec
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Best Local Similarity 98.4%;
Matches 123; Conservative
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Best Local Similarity
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                                                                                        TGGAG 50
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98.4%;
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                                                                                                                                                                                                                                                                                                         Gaps
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Title:
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Maximum Match 100%
Listing first 45 summaries
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   length: 0
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Match
 US-09-834-291-2_COPY_1_125
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/6B_COMB.seq: *
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US-09-339-964-1
US-09-318-978-10
US-09-318-978-10
US-09-017-706-3
US-09-017-706-6
US-09-017-706-6
US-09-017-706-7
US-09-017-706-7
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US-09-08-487-811A-12
US-09-060-694-12
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RESULT 2  US-09-428-517-1/c  Sequence 1, Application US/ Patent No. 6251636  GENERAL INFORMATION: APPLICANT: Betlach, Mary C APPLICANT: Shah, Sanjay Ki; APPLICANT: Tang, Li APPLICANT: Tang, Li APPLICANT: TONE RECOME TITLE OF INVENTION: RECOME FILE REFERENCE: 30062-2002 CURRENT FILING DATE: 1999; EARLIER APPLICATION NUMBER CURRENT FILING DATE: 1999;	Jari Jons 1411 1411 1419 1499 1499	ESULT 1 Sequence 1, Application US/C Patent No. 6025198 GENERAL INFORMATION: APPLICANT: C. Frank Bennett APPLICANT: Lex M. Cowsert TITLE OF INVENTION: ANTISEN FILE REFERENCE: RTS-0065 CURRENT FILING DATE: 1999- UNUMBER OF SEQ ID NOS: 47 SEQ ID NO 1 LENGTH: 4743 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (212)(3988)	21.6 21.6 21.6 21.6 21.6 21.6 21.6 21.6
ion US/094285 Mary C. njay Krishnak , Robert RECOMBINANT 62-20029.00 NUMBER: US/0 : 1999-10-28 : 1999-02-16	29.3%; Score ty 58.9%; Pred. ervative 0; Mi aggcggggcagctccggc               ctgaaccacagcggaattga                       gtgtccgtccggaaatga	on US/09 Bennett wsert ANTISENS NUMBER: 1999-06 : 47 ens	921 921 921 921 1413 4157 4157 4157 2362 2362 2362 3319 3319 3319 3319 3319 3319 3319 331
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709428517 2: :ishnakant rt 3: :INANT OLEANDOLIDE 29.00 29.00 29.00 29.00 29.00 29.07 20.02 20.02 20.02 20.02 20.02 20.02	Score 36.6; Pred. No. () ; Mismatch ; Mismatch ; Hill jaggagctccs attgaagcgga i           jaggagctccs attgaagcgga	39964 MODULATION OF 18/09/339,964	US-08-396-650-3 US-08-396-650-4 US-08-768-626-3 US-08-768-626-4 US-08-162-146-2 US-08-162-146-2 US-09-314-127-2 US-09-231-718-8 US-09-232-200-48 US-09-232-201-48 US-09-232-201-48 US-09-232-201-48 US-09-232-201-48 US-08-282-845-1 US-08-282-845-1 US-08-430-225A-19 US-08-430-225A-19 US-08-430-225A-19
e POLYKETID	DB 3; I 031; ss 44; sgagaccac          taagacctc  tagacctc	SHIP-2	1
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EARLIER FILING DATE: 1999-02-16

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                 US-09-017-706-3
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; OTHER INFORMATION: Description of Artifical Sequence: Recombinant DNA
US-09-428-517-1
Sequence 3, Application US/09017706A
                                                                                                                                                                                                                              Matches
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LENGTH: 50937
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kaser, Matthew, R.
APPLICANT: Baughn, Mariah, R.
TITLE OF INVENTION: LIFID METABOLISM TRANSCRIPTION FACTOR
FILE REFERENCE: PC-0004 US
CURRENT APPLICATION NUMBER: US/09/318,978A
CURRENT FILING DATE: 1999-05-26
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PERL Program
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LOCATION: 186, 189, 195, 196, 200, 204, 208, 2
NAME/KEY: unsure
LOCATION: 228, 236, 244, 248, 251
OTHER INFORMATION: a or g or c or t, unknown,
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SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29900 GATGGCGATCGGCTCTCGGGCCCCGTTCCTCGGTCTCGCGGAGTCGATCGCTGACCTCCTT 29841
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ORGANISM: Homo sapiens
FEATURE:
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Pred. No. 3.8;
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                                                                                                                                                                                                                                                           SOFTWARE: 1
SEQ ID NO 4
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Best Local Similarity
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APPLICANT: ITO, YOSHIFUMI
APPLICANT: ITO, YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND
TITLE OF INVENTION: TRANSFORMANT
FILE REFERENCE: 8361-0003-0
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND FITLE OF INVENTION: TRANSFORMANT FILE REFERENCE: 8361-0003-0
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                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 14
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EARLIER APPLICATION NUMBER: JP 305071/1997
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                                                                                                                       NAME/KEY: CDS
LOCATION: (7)..(1848)
                                 LOCATION: (85)..(1848)
OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
                                                                                                                                                                                          TYPE: DNA
ORGANISM: Pseudomonas
OTHER INFORMATION: MUTATED GENOMIC DNA
                                                              NAME/KEY: mat_peptide LOCATION: (85)..(1848
                                                                                                         FEATURE:
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NAME/KEY: CDS
LOCATION: (7)...(1848)
                        FEATURE
                                                                                                                                                                                                                                     LENGTH: 1981
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OTHER INFORMATION: MUTATED GENOMIC DNA
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LOCATION: (85)..(1848)
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Pred. No. 10;
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; OTHER INFORMATION: PLASMID POS3410H57
US-09-017-706-4
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                                                           Sequence 6, Application US/09017706A Patent No. 6087147 GENERAL INFORMATION:
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NAME/KEY: mat_peptide

TOTATION: (85)...(1848)
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND
                                         APPLICANT: ITO, YOSHIFUMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (85)..(1848)
OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (7)..(1848)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1451 gatgcaggcggccacgcgatgctgtccgcacccgcttatggcgcggcggcgatccacgtc 1510
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                                                                                                                                                                                                                                                                                               1451 gatgcaggcggccacgcgatgctgtccgcacccgcttatggcgcggcggcgatccacgtc 1510
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                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                           1 gatcccgctgggcaggcgggggcagctccgggcgctcctcggagaccactgcgctccacgtt 60
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                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Score 27.8; |
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 1981;
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; OTHER INFORMATION: PLASMID: pOS3410H139 US-09-017-706-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-017-706-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09017706A Patent No. 6087147
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Best Local :
                                                                                                                                                                                                                                                                                                                       SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: TRANSFORMANT
FILE REFERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: JP 305071/1997
EARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A-ANTLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND TITLE OF INVENTION: TRANSFORMANT FILE REPERENCE: 8361-0003-0 CURRENT APPLICATION NUMBER: US/09/017,706A CURRENT FILING DATE: 1998-02-05 EARLIER APPLICATION NUMBER: JP 305071/1997 EARLIER FILING DATE: 1997-10-21 NUMBER: OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ITO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: mat_peptide
                                                                                                      NAME/KEY: mat_peptide LOCATION: (85)..(1848) OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (7)..(1848)
                                                                                                                                                                                                                                                                                 TYPE: DNA
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NAME/KEY: CDS
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                                            FEATURE
                                                              OTHER INFORMATION: MUTATED GENOMIC DNA
                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                        FEATURE:
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                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                     LENGTH: 1981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.2%;
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Pred. No. 10;
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Query Match

22.2%;

Score 27.8;

DB 3;

Length 1981;

Best Local Similarity

54.4%; Pred. No. 10;

COUNTRY: Canada

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RESULT 10
US-08-623-471-8/c
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Best Local Similarity
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LENGTH: 1
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Patent No. 6087147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND TITLE OF INVENTION: TRANSFORMANT FILE REFERENCE: 8361-0003-0 CURRENT APPLICATION NUMBER: US/09/017,706A CURRENT APPLICATION NUMBER: US/09/017,706A CURRENT FILLING DATE: 1998-02-05 EARLIER APPLICATION NUMBER: JP 305071/1997 EARLIER FILING DATE: 1997-10-21 NUMBER: JP 305071/1997 EARLIER FILING DATE: 1997-10-21 NUMBER OF SEQ ID NOS: 14
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OTHER INFORMATION: MUTATED GENOMIC DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: mat_peptide LOCATION: (85)..(1848)
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LOCATION: (7)..(1848)
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                                                   APPLICANT: Kamboj, Rajender
TITLE OF INVENTION: STABLE D4 CELL LINES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                APPLICANT: Allelix Biopharmaceuticals Inc
APPLICANT: Owolabi, Joshua
APPLICANT: Rampersad, vikarna
APPLICANT: Kamboj, Rajender
                                                                                                                                                                                                                                                                                                                            1511 ggtgcgcgcatcggcgacacgcagcaggtgcagcagtgctcag 1553
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CITY:
                    STREET:
                                  ADDRESSEE:
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Mississauga
          3: Allelix Biopharmaceuticals Inc 6850 Goreway Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.2%; 54.4%;
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Pred. No. 10;
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RESULT 11
US-07-928-611-12/c
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Patent No. 5569601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
ATTURNEL, NO. 5569601nan, Kevin E NAME: NO. 5569601nan, Kevin E REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 19920810 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Van Tol, Hubert H.M.
APPLICANT: Civelli, Olivier
TITLE OF INVENTION: A No. 5569601el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 27-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: RIDOUT & MAYBEE, Attn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: PCT/CA94/00538
PTI.TNG DATE: 27-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: AL TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 CCGGGCGCGGGGGCGCACAGTCGGGGCCGCAGGGGTCCGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                               USA
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Pred. No. 8;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                      APPLICANT: Civelli, Olivier
APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: A No. 5883226el Human Dopamine
NUMBER OF SEQUENCES: 24
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/evidence= EXPERIMENTAL
/rpt_unit= 346 .. 394
/rote= "This sequence is a repeat found in 7 known
alleles of the human D4 dopamine receptor gene
encoding a 16 amino acid sequence repeated 7 times
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Pred. No. 9.7;
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US-08-487-811A-12
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Best Local :
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NAME: NO. 5883226nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,
TELECCOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US
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501 CCGGGCGCGGGGGCGCACAGTCGGGGCCGCAGGGGTCCGGG
                65 -tgggcgtggggggggacaggaattgaagcggaagtctggg 105
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                                                                                                                                                           Local Similarity
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LOCATION:
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CLASSIFICATION:
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/evidence= EXPERIMENTAL
/rpt_unit= 346 .. 394
/rpt= "This sequence is a repeat found in 7 known
alleles of the human D4 dopamine receptor gene
encoding a 16 amino acid sequence repeated 7 times
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/standard_name= "Alternate Exon 3: D4.7"
/note= "This sequence represents the third exon
allele D4.7 of the human D4 dopamine receptor
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/function= "PstI site"
/evidence= EXPERIMENTAL
/standard_name= "PstI site"
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Sequence 12, APP--
Sequence 12, APP---
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APPLICANT: Van Tol, Hubert H.M.
APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: A NO. 6203998el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 6203998nan, Kevin
REGISTRATION NUMBER: 35,303
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LENGTH: 803 base pairs
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OTHER
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CITY: Chicago
                                                                    NAME/KEY:
                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                        OTHER INFORMATION:
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                                      LOCATION:
                                                                                                                                                                                   INFORMATION:
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/label= PstI
/label= PstI
/note= "This sequence is a PstI site whereby
digestion of human genomic DNA produces a RFLP"
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/standard_name= "Alternate Exon 3: D4.7"
/note= "This sequence represents the third exon of allele D4.7 of the human D4 dopamine receptor
                                                                                                                                         /note= "This sequence is a repeat found in 7 known alleles of the human D4 dopamine receptor gene encoding a 16 amino acid sequence repeated 7 times
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/evidence= EXPERIMENTAL
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/rpt_unit= 346 .. 394
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PCT-US93-07370-12
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                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 803 base pairs
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                                                                                                                       FEATURE:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 CCGGGCGCGGGGGGCGCACAGTCGGGGCCGCAGGGGTCCGGG
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OTHER INFORMATION: /si
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SOFTWARE: Patentin
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LOCATION:
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22.1%;
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                                                                                                                                                    OD: experimental
/rpt_type= "tandem"
/evidence= EXPERIMENTAL
/rpt_unit= 346 . . 394
/note= "This sequence is a repeat found in 7 known alleles of the human D4 dopamine receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Release #1.0, Version #1.25
                                                                                                                                encoding a 16 amino acid sequence repeated 7 times
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/note= "This sequence is a PstI site whereby
digestion of human genomic DNA produces a RFLP"
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/evidence= EXPERIMENTAL
/standard_name= "Alternate Exon 3:
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                                                                                                                                                                                                                                                                                                                                                                                /evidence= EXPERIMENTAL
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Score 27.6; DI
Pred. No. 9.7;
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Pred. No. 9.7;
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                 DB 5;
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                 Length 803;
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; Sequence 5, Application US/08056051

; Patent No. 5516683
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/056,051
FILING DATE: 1930429
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5516683nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1234
TELEPHONE: 312-715-1234
                                                                                                              Matches
                                                                                                                            Query Match
Best Local Similarity
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 5:
                                    1062 CCCCGGGAAGGCCGGGGGGGGGGGGCGCACAGGGGGTCCTGGGGGAGG 1003
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APPLICANT: Van Tol, Hubert H.-M.
TITLE OF INVENTION: A NO. 5516683el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       FEATURE:
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CITY: Chicago
STATE: Illinois
65 -tgggcgtggggggggacaggaattgaagcggaagtctggg 105
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1610 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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                                                       5 ccgctgggcaggcgggcagctcctgggagaccactgcggtccacggttgagg 64
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10 South Wacker Drive, Suite 3000
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                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grandy, David K
Bunzow, James R
                                                                                                                                                                                                                                                                                                                      5'UTR
1..103
                                                                                                                                                                                                                                                                     3'UTR
1508..1610
                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                 104..1507
                                                                                                                           22.1%; 60.8%;
                                                                                                        ; Score 27.6; DB 1;
; Pred. No. 11;
0; Mismatches 39;
                                                                                                          39;
                                                                                                                                         Length 1610;
                                                                                                        Indels
                                                                                                          1;
                                                                                                      Gaps
                                                                                                          1;
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Db 1002 CCGGGCGCGGGGGCCACAGTCGGGGCCCAGGGGTCCGGG 961

Search completed: September 7, 2002, 18:23:12 Job time: 28886 sec

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Title:
Perfect score:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
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    987654321
                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                              Score
  125
36.6
32.8
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 1.0
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125
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1: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA199.DAT: *
2: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA199.DAT: *
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4: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1994.DAT: *
5: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1995.DAT: *
6: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1995.DAT: *
7: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1995.DAT: *
9: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT: *
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2: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT: *
2: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT: *
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gatcccgctgggcaggcggg.....aagctttagggtcgctggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
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  266
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AAZ88700
AAZ91408
AAC81955
AAIG87271
AAS29777
AAL01443
AAC44059
AAK92251
AAK92251
                                                                                                                                                                                                                                                        SUMMARIES
                    Human cytoskeletal
Human reproductive
Zea mays DNA fragm.
Human cDNA 5'-end
                                                                                                                                                                                            Description
                                                                                                                                     Human CD95 recepto
Human Ship-2 nucle
                                                                                              Human Meg-3 cDNA.
Human osteoclast e
  Human cDNA clone
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DNA encoding novel	AAS85776 AAS89212	233	1371 1372	23.5	29.4 29.4	44
encoding nove	AAS77912	23	1371	ω	29.4	43
encoding nove	•	23	1371	w	29.4	2
s sys	ABA16261	22	19115	w	29.6	41
Human immune/haema	U.	22	15554	ω	29.6	0
ന	ሥ	22	3665	ω	29.6	39
Zea mays DNA fragm	AAC44492	21	1769	ω	29.6	38
an secrete	AAD05562	22	1551	w	29.6	37
Drosophila melanog	975	23	4569	ω	29.8	36
	87	22	3593	ω	29.8	35
	AAK94348	22	2410	ω	29.8	34
	AAS76184	23	2244	w	29.8	ω ω
	AAS76156	23	2244	w	29.8	32
-	AAF94082	22	842	w	29.8	3
O	AAK93732	22	776	w	29.8	30
	AAK91993	22	776	ω	29.8	29
Drosophila melanog	ABL19753	23	2262	4	30.6	28
	AAV62142	19	2056	4	30.6	27
tomyces vene	AAT62457	18	1662	4	30.6	26
Human secreted pro	AAX22112	20	1180		30.6	25
2.301 kb SM-MHC-pr	AAT88426	18	2301	-	31	24
3	AAS90936	23	647	G	31.4	23
Genetic construct	AAF76962	22	8537	5	31.6	22
Human liver cell s	AAH57472	22	1758	ر.	31.6	21
Human derived cyto	AAF76957	22	1485	.51	31.6	0
	AAF76954	22	1485		31.6	9
Human derived cyto	AAT17409	17	1485	<u>ر</u>	31.6	8
Human cytochrome P	838	17	1485	.51	31.6	7
Human cytochrome P	AAT28387	17	1485		31.6	5
-(3	AAQ87722	16	1485		31.6	5
Human auxillary cy	AAQ87721	16	1485		31.6	4
Human secreted pro	AAV43618	19	1553	.51	32	ω
. Human full-length	AAK94547	22	1544	.51		ผ
Human reproductive	051	22	1371			Ξ
Human cytoskeletal	82	22	1371			5

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## ALIGNMENTS

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RESULT

AAZ880X

XX AAZ8

AC AAZ8

XX AAZ8

XX Huma

XX Canc

XX Canc

XX Homc

XX Homc

XX Homc

XX Homc

XX DE15

XX O3-F

PD 03-F

PD 03-F

PD 16-C

XX DE6-C

XX D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CD95 receptor intron 1 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ88700 standard; DNA; 266 BP
                                          Krammer P, Mueller-Schilling M, Oren M;
                                                                                                                                                                                                                                16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE19847779-C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer chemotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ88700;
                                                                                                                                (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                 16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                      98DE-1047779
                                                                                                                                                                                                                                                                                                                 98DE-1047779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /bound_moiety= p53
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
Example 13; Column 41-52; 34pp; English
                      Antisense oligonucleotides, useful for inhibiting human Ship-2 expression and for detecting nucleic acids encoding Ship-2 -
                                                                             WPI; 2000-181819/16.
                                                                                                        Bennett CF,
                                                                                                                                                          25-JUN-1999;
                                                                                                                                                                                  25-JUN-1999;
                                                                                                                                                                                                            15-FEB-2000.
                                                                                                                                                                                                                                    US6025198-A
                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                             Human; Ship-2; antisense oligonucleotide; phosphorothioate; detection; inhibition; SH2-containing phosphatidylinositol phosphatase-2; ss.
                                                                                                                                (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                     Human Ship-2 nucleotide sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ91408 standard; cDNA; 4743 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor intron 1 which contains a p53 binding region described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ91408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel p53-binding region of a human CD95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-162245/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 tggag 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 gatocogotgggcaggcagctccggcgctcctcggagaccactgcgctccacgtt 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tggag 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gatcccgctgggcaggcgggcagctccggcgctcctcggagaccactgcgctccacgtt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9a9gt9g9gcgt9g9ggggggacaggaattgaagcggaagtctgggaagctttagggtcgc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125;
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                                                                                                        Cowsert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                        99US-0339964
                                                                                                                                                                                99US-0339964.
                                                                                                                                                                                                                                                                                    Location/Qualifiers 212..3988
                                                                                                                                                                                                                                                          /product= "Ship-2"
                                                                                                                                                                                                                                                                         /*tag=
                                                                                                        Ĭ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Pred. No. 2.2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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CCC XXX PT XXX
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AAC81955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                        Claim 4; Page 44-53; 65pp; Japanese
                                                                    {\tt Meg-3} protein expressed in mesangial kidney cells for diagnosis treatment of kidney disease -
                                                                                                                   P-PSDB; AAB11456.
                                                                                                                                 WPI; 2000-687536/67.
                                                                                                                                                               Miyata T;
                                                                                                                                                                                                                                         30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meg-3; human; mesangial kidney cell; treatment; diagnosis; renal; antidiabetic; vaccine; gene therapy; pathogenesis; kidney disease; glomerulonephritis; diabetes; proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes phosphorothioate antisense oligonucleotides that specifically hybridise with, and inhibit the expression of, nucleic acids encoding human Ship-2 (also called SH2-containing phosphatidylinositol phosphatase-2). Also described is a method of inhibiting the expression of Ship-2 in human cells or tissues in vitro comprising contacting the cells with the phosphorothioate antisense oligonucleotides. The phosphorothioate
                                                                                                                                                                                           (MIYA/) MIYATA T.
                                                                                                                                                                                                                                                                   28-APR-2000; 2000WO-JP02831
                                                                                                                                                                                                                                                                                                                               W0200066729-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meg-3; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Meg-3 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC81955 standard; cDNA; 3768 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4408 ggtgggggggggtgtccgtccggaaatgaaggaatagcccgaggacc 4454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4348 ttccaccgggcctgaaccacagcggaggagctccgctaagacctccccacccccgctggg 4407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense oligonucleotides can be used to treat animals (especially humans) suspected of having or being prone to a disease or condition associated with Ship-2 expression. The present sequence encodes
                                                                                                                                                                                                           (KURO/) KUROKAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC81955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4743 BP; 939 A; 1466 C; 1448 G; 890 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human Ship-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ggfgggcgfggggggggaagtggaattgaagcggaagtctgggaagc 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 tecegetgggeaggegggegeteeteggagaecaetgegeteeaegttga 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                         99JP-0123561
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 53..2254
                                                                                                                                                                                                                                                                                                                                                           /product= "Meg-3"
                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.3%;
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This invention describes a novel protein highly expressed in mesa kidney cells which has renal and antidiabetic activity and which

mesangial

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RESULT
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                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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                                                                                                                                                                                                                                                                                                                                                                                          JP2001231573-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; osteoclast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI68201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI68201 standard; cDNA; 3995 BP
                                                                                                                         The invention relates to human osteoclast expressed polynucleotide sequences (AAI68200-AAI68203) and the encoded proteins (AAMS1208-AAMS1211). The polynucleotides are useful as an index formaturation of osteoclasts.
                                                                                                                                                                                                                                                                                                               21-FEB-2000; 2000JP-0048886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2001 (first entry)
                                                                                                 Sequence 3995 BP;
                                                                                                                                                                                      Claim 1; Page 14-18; 31pp; Japanese.
                                                                                                                                                                                                                                                                                       (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  763 ggcagagctcggcccgcggctgaaggggaaaccgcaggagcggcagcggcagtgga 818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
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9 tgggcaggggggagctccgggggctcctcggagaccactgcgctccacgttgaggtggg
                                                                                                                                                                                                               osteoclasts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgtggggggcggacaggaattgaagcggaagtctgggaagctttagggtcgctgga 124
                                                                                                                                                                                                                                                                2001-609964/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
                                                                                                                                                                                                                        derived from human osteoclast, used as
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                                                  Similarity
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                                     Conservative
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/product= "osteoclast expressed protein"
                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                 755 A; 1222 C; 1308 G; 710 T; 0 other;
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55.2%;
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Pred. No. 3.
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative;
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AAS29777 standard; cDNA; 1110
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02-MAR-2000;
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26-JUL-2000;
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14-JUL-2000;
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07-JUL-2000;
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07-JUN-2000;
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17-MAR-2000;
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14-AUG-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regeneration; anti-infertility; food additive.
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2000US-0226279
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2000US-0217487.
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01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000;

2000US-0229287. 2000US-0229343. 2000US-0229344. 2000US-0229345. 2000US-0229519. 2000US-0229513. 2000US-0230437. 2000US-0230438. 2000US-0231243. 2000US-0231243. 2000US-0231244. 2000US-0231244. 2000US-0231244.

08-SEP-08-SEP-12-SEP-

14-SEP-14-SEP 14-SEP

2000US-0232400. 2000US-0232401. 2000US-0232398. 2000US-0232399. 08-SEP-

08-SEP-

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                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated human cytoskeletal element-related polypeptide useful for diagnosis/treatment of neoplastic disorders, disorders associated with neural transmission, chromosomal abnormalities, autoimmune
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17-NOV-2000;
17-NOV-2000;
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63 ggtgggcgtggggggggacaggaattgaagcggaagtctgggaagctttagggtcgctg 122
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                                                                     tcccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgttga 62
                                             TGCCGCTGGCCAGGAGCAGCTGCATGAGGAGCTCCGTGATGTCCCTGCCCGCCACGTGGA
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                                                                                                                                  Conservative
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2000US-0254097.
2001US-0259678.
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2000US-0251869.
2000US-0251989.
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2000US-0251479.
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2000US-0250391.
2000US-0251030.
2000US-0251988.
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2000US-0249213.
2000US-0249214.
2000US-0249215.
2000US-0249216.
2000US-0249217.
2000US-0249218.
2000US-024924.
2000US-024924.
2000US-024924.
2000US-0249265.
2000US-0249265.
2000US-02492929.
2000US-0249290
                                                                                                                                                                                                              data for this patent did not form part of the printed
                                                                                                                                                   25.9%;
                                                                                                                                Score 32.4; DB 22; Length 1110;
Pred. No. 4;
0; Mismatches 56; Indels 0;
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29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000

2000US-0236369 2000US-0236370

2000US-0236327

14-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000;

02-OCT-2000; 13-OCT-2000; 13-OCT-2000; 20-OCT-2000; 20-OCT-2000;

2000US-0240960. 2000US-0241221. 2000US-0239935. 2000US-0239937.

2000US-0241785

08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000;

2000US-0246609. 2000US-0246610. 2000US-0246611. 2000US-0246613.

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2000US-0246525. 2000US-0246526. 2000US-0246527.

2000US-0246528 2000US-0246532

2000US-0246478. 2000US-0246523. 2000US-0246524.

17-NOV-2000;

20-CCT-2000 20-CCT-2000 01-NOV-2000 08-NOV-2000 08-NOV-2000

2000US-0246475. 2000US-0246476. 2000US-0246477.

2000US-0241786. 2000US-0241787. 2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-0244617. 2000US-0246474.

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	14-SEP 12-SEP 14-SEP 14	08-SEP-2000; 08-SEP-2000;	08-SEP-2000;	08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

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05-DEC-2000;
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05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
          Zea mays subsp. mays.
                                                                                                            Zea mays DNA fragment SEQ ID NO: 41471.
                                                                                                                                                                               AAC44059;
                                                                                                                                                                                                              AAC44059 standard; DNA; 1388
                                                                                                                                           18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1110 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1444; 1297pp + Sequence Listing; English.
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P-PSDB; AAM95473.
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2000US-0249264.
2000US-0249267.
2000US-0249297.
2000US-0249300.
2000US-0250160.
2000US-0250160.
2000US-0251030.
2000US-0251030.
2000US-02518719.
2000US-0251869.
2000US-0251869.
2000US-0251999.
2000US-0251999.
2000US-0251999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.9%;
54.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32.4; DB Pred. No. 4; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
      25-FEB-1999
05-MAR-1999
05-MAR-1999
23-MAR-1999
25-MAR-1999
06-APR-1999
06-APR-1999
06-APR-1999
06-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
24-MAY-1999
06-MAY-1999
06-MAY-1999
14-MAY-1999
14-JUN-1999
14-JUN-1999
18-JUN-1999
23-JUN-1999
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990S-0137502
990S-0138094
990S-0138047
990S-0139452
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990S-0140823
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99US-0127462
99US-0127462
99US-0127462
99US-0128734
99US-0130077
99US-0130510
99US-0130449
99US-0132407
99US-0132484
99US-0132486
99US-0132487
99US-0132487
99US-0134218
99US-0134219
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137724.
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01-JUL-1999 01-JUL-1999 02-JUL-1999 06-JUL-1999 08-JUL-1999 09-JUL-1999 12-JUL-1999 13-JUL-1999 14-JUL-1999 15-JUL-1999

99US-0141842. 99US-0142054. 99US-0142390. 99US-0142390. 99US-0142803. 99US-014297. 99US-0142977. 99US-0143542. 99US-0143542.

19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;

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990S-0144085
990S-0144085
990S-0144325
990S-0144331
990S-0144333
990S-0144333
990S-0144814
990S-0145088
990S-0145088
990S-0145218
990S-0145236
990S-0151303
990S-0151303
990S-0151303
990S-0153363
990S-0153363
990S-0153363
990S-0153363
990S-0153363
RESULT 8
AAK92251/c
ID AAK92251;
XX
AC AAK92251;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human cDNA 5'-end sequence, SEQ
XX
DE Human; full length cDNA; cDNA s
XX
OS Homo sapiens.
XX
PD EP1130094-A2.
XX
PD 05-SEP-2001.
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                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                        07-OCT-1999
08-OCT-1999
11-OCT-1999
13-OCT-1999
13-OCT-1999
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21-OCT-1999
22-OCT-1999
22-OCT-1999
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26-OCT-1999
28-OCT-1999
28-OCT-1999
28-OCT-1999
28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1999
20-SEP-1999
22-SEP-1999
23-SEP-1999
24-SEP-1999
28-SEP-1999
29-SEP-1999
05-OCT-1999
06-OCT-1999
                                                                                                 Human cDNA 5'-end sequence, SEQ ID
                                                                            Human; full length cDNA; cDNA synthesis; oligo-capping;
                                                                                                                                                                                                                                                     94 CGAGACGGGATGGACGGGACGGGAGGGGATCGGAATCGTCG
                                                                                                                                                                                                                             79 ggacaggaattgaagcggaagtctgggaagctttagggtcg
                                                                                                                                                                                                                                                                                               25.8%;
l Similarity 57.4%;
58; Conservative
                                                                                                                                                                                                                                                                                                                                         990S-0154039
990S-0154799
990S-0155486
990S-0155596
990S-015596
990S-015596
990S-0157765
990S-0159293
990S-0159293
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990S-0159293
990S-0159329
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990S-0159331
990S-0159637
990S-0159637
990S-0160761
990S-0160761
990S-0160761
990S-0160980
990S-0161406
990S-0161359
990S-0161406
990S-0161359
990S-0161361
990S-0161361
990S-0161361
990S-0161361
990S-0161392
990S-0161392
                                                                                                                                                                                                                                                                                               score 32.2; DB; Pred. No. 4.7; O; Mismatches
                                                                                                                                                               ВP
                                                                                                   NO: 711.
                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                  0;
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Gaps

0;

22-JUL-1999
22-JUL-1999
23-JUL-1999
23-JUL-1999
23-JUL-1999
23-JUL-1999
23-JUL-1999
26-JUL-1999
27-JUL-1999
28-JUL-1999
28-JUL

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RESULT 9
AAK93511/c
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Best Local
                                         08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
            (HELI-) HELIX RES INST
                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                       Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                         Human cDNA clone representative sequence, SEQ ID NO: 1971.
                                                                                                                                                                                                                                                                                                                        AAK93511;
                                                                                                                                                                                                                                                                                                                                                   AAK93511 standard; cDNA; 511 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to primers for synthesising full length cD clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                     07-JUL-2000;
                                                                                                                                     05-SEP-2001
                                                                                                                                                                   EP1130094-A2
                                                                                                                                                                                                                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 511 BP; 77 A; 173 C; 180 G; 78 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-1999; 99JP-0194486
11-JAN-2000; 2000JP-0118774
02-MAY-2000; 2000JP-0183765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUL-2000; 2000EP-0114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                            249 AGGTGGGCAGCGGGGCAGCGCGTGGCCAGACCGCGGGGCAGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 CCGCGGGGCAGACGCGGCAACAGCGGCACAGGTCGAACACCGGCGTGGTCCCCCAGCGCGC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 tgggcgtgggggggggacaggaattgaagcggaagtctggggaagctttaggg 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loca I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        υı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primers useful for synthesizing full length cDNA clones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccgctgggcaggcgggcagctccgggggagaccactgcgctccacgttgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic manipulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 711; 1380pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                         99JP-0194486.
2000JP-0118774.
2000JP-0183765.
                                                                                                     2000EP-0114089
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0194486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.6%;
55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T, Hayashi K,
a T, Nagai K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nii S, Kawai Y;
Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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RESULT 10
AAS29822
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Best Local
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                     cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancerial; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; sastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative; tissue regeneration; anti-infertility; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clones. 830 cDNA molecules encoding a human protein have been isolated and nuclectide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                          17-JAN-2001; 2001WO-US01331.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytoskeletal element-related protein; human; mouse; rabbit;
                                                                                                                                                            WO200155168-A1
                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytoskeletal element-related polypeptide encoding genomic DNA #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS29822 standard; DNA; 1371 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 511 BP; 77 A; 173 C; 180 G; 78 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ota T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 11; SEQ ID NO 1971; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-524255/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 CCGCGGGGCAGACGCGGCAACAGCGGCACAGGTCGAACACCGGCGTGGTCCCCAGCGCGC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 tgggcgtgggggggggaacaggaattgaagcggaagtctgggaagctttaggg 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 55.4 ses 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primers useful for synthesizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGTGGGCAGCGCGGGGCAGCGCGTGGGCTGGCAGACCGCGGGGCAGGAGGG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccgctgggcaggcggggcagctccgggagaccactgcgctccacgttgagg 64
2000US-0179065.
2000US-0180628.
2000US-0184664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.6%;
55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T,
na T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ai T, Hayashi K,
Nagai K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hii S, Kawai Y;
Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                      goat; horse;
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0

07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 07-JUL-2000; 11-JUL-2000;

18-APR-2000; 19-MAY-2000; 2-MAR-2000; 6-MAR-2000; 7-MAR-2000;

11-JUL-2000; 14-JUL-2000; 26-JUL-2000;

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17.NOV-2000;
01.DEC-2000;
05.DEC-2000;
05.DEC-2000;
05.DEC-2000;
05.DEC-2000;
06.DEC-2000;
08.DEC-2000;
08.DEC-2000;
08.DEC-2000;
08.DEC-2000;
08.DEC-2000;
08.DEC-2000;
08.DEC-2000;
08.DEC-2000;
08.DEC-2000;
09.DEC-2000;
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13-CCT-2000

20-CCT-2000

20-CC
Claim
                                            disorders
                                                             Novel isolated human cytoskeletal element-related pol
for diagnosis/treatment of neoplastic disorders, disorters, disorters, disorters, disorters, with neural transmission, chromosomal abnormalities,
                                                                                                                                                                                                                                                (HUMA-)
                                                                                                                                                         2001-476182/51.
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SEQ
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2000US-0239935.
2000US-0239935.
2000US-0244785.
2000US-0241786.
2000US-0241826.
2000US-0244676.
2000US-0246476.
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2000US-0251868.
2000US-0251989.
2000US-0254099.
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2000US-0254099.
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2000US-0254099.
2000US-0254099.
ID
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No
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107;
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                                                                                                                                                                                                      Ruben
505pp; English
                                                                                                                                                                                                        SM;
                                                                                    d polypeptide useful disorders associated
                                                                                         associated
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מאסים שים סיסים סיסים סיסים סיסים סיסים סיטים סיסים סיסים סיסים או מאסים או מאסים מאסים

2000US-0186350 2000US-019974 2000US-019975 2000US-0214867 2000US-0216847 2000US-0216847 2000US-0216847 2000US-0217487 2000US-0217487 2000US-0217487 2000US-0217487 2000US-0217487 2000US-0228514 2000US-0228514 2000US-0228575 2000US-02285681 2000US-02285681 2000US-02285681 2000US-02285681 2000US-02285681 2000US-0228509 2000US-0228509 2000US-0228509 2000US-0228509 2000US-0231444 2000US-0231443 2000US-0231444 2000US-0231468 2000US-0233463 2000US-0233463 2000US-0233463 2000US-02335844 2000US-02335849 2000US-02335849 2000US-02335844 2000US-

30-AUG-2000; 01-SEP-2000; 01-SEP-2000;

14 - AUG - 2000; 14 - AUG - 2000; 18 - AUG - 2000; 22 - AUG - 2000; 22 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 65
                                                             04 - FEB - 2000;
24 - FEB - 2000;
02 - MAR - 2000;
16 - MAR - 2000;
17 - MAR - 2000;
19 - APR - 2000;
19 - MAY - 2000;
07 - JUN - 2000;
30 - JUN - 2000;
07 - JUN - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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3199/c
AAL05199 standard; DNA; 1371 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAS29814-AAS29838 represent genomic DNA molecules, which encode the cytoskeletal element-related polypeptides of the invention. Cytoskeletal polypeptides and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders
                                                                                                                                                                                                                                                                                            31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                  17-JAN-2001; 2001WO-US01339
                                                                                                                                                                                                                                                                                                                                                                                                                 WO200155320-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human reproductive system related antigen DNA SEQ ID NO: 7887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; {\tt ds}.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccgctggccaggagcagctgcatgaggagctccgtgatgtccctgcccgccacgtggagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65;
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                     2000US-0180628
2000US-018464
2000US-0186350
2000US-0189874
2000US-0199076
2000US-0199123
2000US-020515
2000US-0205467
2000US-0214886
2000US-0215135
2000US-0216880
2000US-0216880
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Pred. No. 5.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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    14-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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25-CCT-2000;
26-CCT-2000;
27-CCT-2000;
28-CCT-2000;
29-CCT-2000;
20-CCT-2000;
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18 - AUG - 2000;
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2000US-0239935
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2000US-0236370.
2000US-0236802.
2000US-0237038.
2000US-0237039.
2000US-0237039.
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2000US-0227009
2000US-0228924.
2000US-0229343.
2000US-0229345.
2000US-0229345.
2000US-0229513.
2000US-0229513.
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2000US-0229513.
2000US-0231242.
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2000US-0231414.
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2000US-0231968.
2000US-0232397.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0236327
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2000US-0235834
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2000US-0232401
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2000US-0220963
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Best Local Similarity
                     Query Match
  Matches
                                                                   The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-2000;
17-NOV-2000;
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17-NOV-2000
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                                                                                                                                Disclosure; SEQ ID NO 7887; 1297pp + Sequence Listing;
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17-NOV-2000
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17-NOV-2000;
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                                                  Sequence 1371 BP; 267 A; 406 C; 430 G;
                                                                                                                                                             Isolated nucleic acid molecule encoding a reproductive system antigen
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                                                                                                                                                                                  2001-465570/50
  65;
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                                                                                                                                                                                                                         HUMAN GENOME
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2000US-0246609
2000US-0246610
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2000US-0246613
2000US-0249208
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2000US-0249299.
2000US-0249300.
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           25.6%;
  0;
           Score 32; DB Pred. No. 5.4;
                                                                                                                                                                                                      SM:
  Mismatches
                                                 268 T; 0 other;
                    DB 22;
  55;
                    Length 1371;
  Indels
                                                                                                                                English
  0;
Gaps
  0;
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ccgctgggcaggcggggcagctccggcgctcctcggagaccactgcgctccacgttgagg 64

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CCGCGGGGCAGACGCGGCAACAGCGGCACAGGTCGAACACCGGCGTGGTCCCCAGCGCGC 250

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249

AGGTGGGCAGCGGGGCAGCGCGTGGGCTGGCAGACCGCGGGGCAGGAGGG tgggcgtggggggggacaggaattgaagcggaagtctgggaagctttaggg 116

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AAK94547/c
 Matches
              Query Match
Best Local
                                                                                                The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                               830\ \mathrm{Primers} useful for synthesizing full length cDNA clones and their use in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID NO 3439; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUL-2000; 2000EP-0114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; full length cDNA; cDNA synthesis; oligo-capping;
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                                                                         Sequence 1544 BP; 332 A; 381 C; 471 G; 360 T; 0 other;
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               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccgctgggcaggcgggcagctccgggcgctcctcggagaccactgcgctccacgttgagg
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                                                                                                                                                                                                                                                                                                                                                                                             2001-524255/58.
 62;
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Conservative
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              25.6%;
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1 T, Nagai K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1544
 0;
              Score 32; DB Pred. No. 5.4;
 Mismatches
                             22;
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3, Otsuki T,
                             Length 1544;
   Indels
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   0
 Gaps
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RESULT 13
AAV43618/c
ID AAV436

AAV43618 standard; DNA; 1553 BP

AAV43618

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CC biological activities, such as cytokine, cell proliferation, or cellular cdifferentiation activities, tissue growth or regeneration, activin or comprehensive activity, chemotactic or chemokinetic activity, haemostatic or comprehensive activity, receptor/ligand activity, tumour inhibition, or comprehensive activity. The proteins can also be used as comprehensive activity. The proteins can be used as comprehensive activity activity. The proteins or cell types which expression. They comprehensive activity activity activity activity activity activity activity activity activity. The proteins can be used in protein interaction in protein expression. They can be used in protein interaction assays, to identify ligands or binding comprehens. Compounds which affect the biological activities of the proteins. Compounds which affect the biological activities of the comprehension of the proteins and comprehension of the protein assays. The proteins and comprehension of the protein activities of diseases which and the protein activities activities and the protein activities of diseases which activities activities and the protein activities of diseases which activities activities activities and the protein activities and the protein activities activities and the protein activities activities and activities and activities and activities activities and activities and activities activities and activities activities and activities activities activities and activities activit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This DNA encodes a human secreted protein. The specification provides secreted protein sequences (AAW63691 to AAW63699) encoded by the nucleic acid sequences shown in AAV43611 to AAV43619. The invention provides a method of identifying a secreted polypeptide which is modified by rough microsomes. The secreted proteins can be used in assays to determine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted human polypeptides - having cytokine, cell proliferation differentiation, activin or inhibin, tumour inhibition or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                             Sequence 1553 BP; 348 A; 384 C; 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Pages 45-46; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-inflammatory activities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-DEC-1997;
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25.6%;
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DB 19;
5.4;
                                                                                        354 T; 0 other;
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                 Length 1553;
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Query Match Best Local Similarity

25.3%; 58.5%;

Score 31.6; Pred. No. 7;

DB 16;

Length 1485;

Sequence 1485 BP; 327 A; 430 C; 413 G; 315 T; 0 other

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                                                          auxillary cytochrome P450 species 2A6. The gene encodes a protein of 494 amino acids. The cDNA was amplified by PCR using the primers AAQ87751-4. The product was cloned into the yeast expression vectors pAAH5N or pAHRR to produce the vectors p2A6 for the expression of the cytochrome P450 alone or p2A6R for co-expression with the yeast NADPH-P450 reductase. The vectors are used in a method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly produced human cytochrome P450 molecular species IA2 (AAQ87714), 2C9 (AAQ87715), 2E1 (AAQ87716), or 3A4 (AAQ87717) or their auxillary species and variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused protein or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for determining whether the chemical compound, or its metabolite, will be
                                              converted into a carcinogenic or mutagenic form through metabolism in the
                                                                                                                                                                                                                                                                                     The nucleotide sequence of the cDNA coding region for the human
                                                                                                                                                                                                                                                                                                                   Examples; Page 49-51; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                     expressing human cytochrome p450 and a yeast NADPH-P450 reductase
                                                                                                                                                                                                                                                                                                                                                                         Evaluation of safety of a chemical cpd. - using recombinant yeast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K,
Yabusaki Y;
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20-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HAYA/) HAYASHI K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGCGGGGCAGACGCGGCAACAGCGGCACAGGTCGAACACCGGCGTGGTCCCCAGCGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko H,
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93JP-0201120.
93JP-0208279.
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The nucleotide sequence of the cDNA coding region for the human CC auxillary cytochrome P450 species 2A6 variant 1. The gene contains a CC change at base 1427 from A to C as compared to the wild type sequence CC (AAQ87721). This changes the amino acid residue from Arg to Lys. The cDNA CC cloned into the yeast expression vectors pAA68 variant 1 for the expression of the cytochrome P450 alone CC vectors p2A6 variant 1 for co-expression of the cytochrome P450 alone CC or p2A6R variant 1 for co-expression with the yeast NADPH-P450 CC a chemical compound by reacting the chemical compound with recombinantly CC (AAQ87715), 2E1 (AAQ87716), or 3A4 (AAQ87717) or their auxillary species and variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused protein or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for determining whether the chemical compound, or its metabolite, will be
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(SUMO ) SUMITOMO CHEM CO LTD.
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20-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko H, Komai K,
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93JP-0201120.
93JP-0208279.
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/note= "G to A change in variant 1 changes amino
acid from Arg to Lys"
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CC converted into a carcinogenic or mutagenic form through metabolism in the CC liver.

XX

SQ Sequence 1485 BP; 328 A; 430 C; 412 G; 315 T; 0 other;

Query Match
Best Local Similarity 58.3%; Score 31.6; DB 16; Length 1485;
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Search completed: September 7, 2002, 18:40:35 Job time: 29929 sec